


```

Db 117 -----GGAAAFDYWGQGLTVTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKD 167
Qy 178 YFPEPVTWNSGALTSVHTTTPAVLQSSGLYSLSVVTVSSSLGTQTYICNVNHNKPSN 237
Db 168 YFPEPVTWNSGALTSVHTTTPAVLQSSGLYSLSVVTVSSSLGTQTYICNVNHNKPSN 227
Qy 238 TKVDKKAEPKSCDKTHTCPDPCAPPELLGSPVFLFPKPKDTLMISRTPEVTCVVDVSH 297
Db 228 TKVDKTKVERKCCVE---CPDPCAPP-VAGPSVFLFPKPKDTLMISRTPEVTCVVDVSH 283
Qy 298 EDEPKFNMYVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKAL 357
Db 284 EDEPKFNMYVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKAL 343
Qy 358 PAPIKTIKAKQPREQVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 417
Db 344 PAPIKTIKAKQPREQVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 403
Qy 418 NNYKTTTPVLDSDGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTOKLSLSPGK 476
Db 404 NNYKTTTPVLDSDGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTOKLSLSPGK 462

RESULT 12
AAR22757
ID AAR22757 standard; Protein: 470 AA.
XX
AC AAR22757;
XX
DT 20-OCT-1992 (first entry)
XX
DE Reshaped CAMPATH-1 antibody heavy chain.
XX
KW Antigen; CD8; complementarity determining region; graft rejection;
KW autoimmune diseases; rheumatoid arthritis; allergy.
XX
OS Rattus rattus.
XX
FH Key
FT Region
FT Region
FT Region
FT Region
FT Peptide
FT Peptide
FT Peptide
FT Peptide
XX WO9205274-A.
XX
XX PD 02-APR-1992.
XX
XX PP 16-SEP-1991; 91WO-GB01578.
XX
XX PR 17-SEP-1990; 90GB-0020282.
XX
XX PA (GORM/) GORMAN S D.
XX
XX PI Clark M R, Cobbold S P, Gorman S D, Waldmann H;
XX
XX DR WPI; 1992-1321139/16.
XX
XX DR N-PSDB; A023570.
XX
XX PT Humanisation of antibodies binding to human CD4 antigen - by
XX mutation of framework-encoding regions of DNA encoding variable
XX domain of rat or mouse antibody chain
XX
XX PS Disclosure; Fig 5; 74pp; English.
XX
XX The sequence is that of the reshaped CAMPATH-1 heavy chain antibody.

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CC Reshaped CD4 antibody can be used to induce tolerance against an
CC antigen. It can also be used to alleviate autoimmune diseases such
CC as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC to a graft, e.g. an organ graft or a bone marrow transplantation can
CC also be useful to alleviate allergies. Tolerance to allergens could
CC also be achieved. See also AAR22754-R22763.
XX
SQ Sequence 470 AA;
Query Match 82.3%; Score 2122; DB 13; Length 470;
Best Local Similarity 86.6%; Pred. No. 2.1e-119;
Matches 408; Conservative 13; Mismatches 40; Indels 10; Gaps 3;
Qy 8 LLLVAAAPRVLSQVLOOMGEGLLQPSSTLSRTCVSGSGISGYVYTWIRQTQPGRLGW 67
Db 8 LFLVATATGVHSQVQLSESGPLVRPSQTLSTCTVSGFTFD-FYNNVVRQPPGRGLEW 66
Qy 68 IGH1--YGNGATTNNPNSLKSRVTISKDTSKNQFNLNLSVTDADTAVVYCARPRDCT 125
Db 67 IGFIRDAKAGYTFEYNPSVKGRTVMTLVDTSKNQFSLSRVTAADTAVVYCARGHHTAAP 126
Qy 126 TICYGWVDVWPGDGLTVTVSSASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPTV 185
Db 127 -----FDYWGQGLTVTVSSASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPTV 179
Qy 186 SNNSGALTSGVHTFPAVLQSSGLYSLSVVTVSSSLGTQTYICNVNHNKPSNTKVDKKA 245
Db 180 SNNSGALTSGVHTFPAVLQSSGLYSLSVVTVSSSLGTQTYICNVNHNKPSNTKVDKKA 239
Qy 246 PKSCDKTHTCPDPCAPPELLGSPVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN 305
Db 240 PKSCDKTHTCPDPCAPPELLGSPVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN 299
Qy 306 WYVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 365
Db 300 WYVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 359
Qy 366 SKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 425
Db 360 SKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 419
Qy 426 VLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTOKLSLSPGK 476
Db 420 VLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTOKLSLSPGK 470

RESULT 13
AAW14927
ID AAW14927 standard; Protein: 467 AA.
XX
XX AC AAW14927;
XX
XX DT 18-OCT-1997 (first entry)
XX
XX DE Human gamma-4PE heavy chain.
XX
XX KW CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
XX cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
XX leukaemia; lymphoma; graft-versus-host disease; asthma;
XX transplant rejection; HIV; therapy; CE9 gamma 4PE.
XX
XX OS Homo sapiens.
XX
XX FH Key
XX FT Location/Qualifiers
XX FT Misc-difference 248 /note= "site of S229P mutation"
XX FT Misc-difference 255 /note= "site of L236E mutation"
XX
XX PN WO9709351-A1.
XX
XX PD 13-MAR-1997.
XX

```

FT Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= signal_peptide
 FT /note= "mouse VH signal peptide sequence encoded by
 FT synthetic linker"
 FT Protein 20..472
 FT /label= heavy_chain
 FT /note= "human gamma 1 chain constant region
 FT and the variable region from anti-rhesus D
 FT antibody D7C2"
 XX
 DN FR2724182-A1.
 XX
 XX
 PD 08-MAR-1996.
 XX
 XX 02-SEP-1994; 94FR-0010566.
 XX
 XX 02-SEP-1994; 94FR-0010566.
 XX
 PA (INSP) INST PASTEUR.
 PA (PROT-) PROTEINE PERFORMANCE.
 XX
 XX Chaabihi H, Edelman L, Kaczorek M, Margaritte C;
 XX
 XX WPI; 1996-162018/17.
 XX N-PSDB; AAT26889.
 XX
 PT Recombinant anti-rhesus D monoclonal antibody - expressed by
 PT baculovirus-transformed insect cells and useful for preventing
 PT haemolysis in new-born babies
 XX
 XX Example 2; Page 35-37; 46pp; French.
 XX
 XX The human monoclonal antibody D7C2, of isotype IgM, recognises a
 CC 30-32 kD polypeptide on the membrane of rhesus positive red blood
 CC cells. The antibody agglutinates rhesus positive cells but not
 CC rhesus negative cells and is useful diagnostically and also for
 CC preventing haemolysis in new-born rhesus positive babies.
 CC Recombinant IGM-D7C2 can be produced by insect cells which have
 CC been transformed by a baculoviral vector comprising a D7C2
 CC expression cassette. The present sequence is that of a recombinant
 CC IGM-D7C2 heavy chain fused downstream of a mouse VH signal peptide.
 XX
 SQ Sequence 472 AA;
 Query Match 86.3%; Score 2223; DB 17; Length 472;
 Best Local Similarity 90.6%; Pred. No. 1.9e-125;
 Matches 425; Conservative 8; Mismatches 32; Indels 4; Gaps 3;
 QY 8 LLLVAAPRWLVLSQVQLQKGGGLLPSETLSRTCTVSGGSGISGYVYWTWIRQTPGRGLEW 67
 DB 8 LFLVATATGVHSQVQLQKGGGLLPSETLSRTCTVSGGSGISGYVYWTWIRQTPGRGLEW 66
 QY 68 IGHYNGGATTNYPNLSKSRVTISKDTSKNOFFFLNLSVTDADTAVYYCARGPRPDCTTI 127
 DB 67 IGEINHSQ-STNYPNLSKSRVTISVDTSKNOFFSLKLSVTAADTAVYYCARA--PEYKWK 123
 QY 128 CYGGWVDVNGPDGLTVSSASTKGSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSW 187
 DB 124 YHGDWFDPMGQGTVTTVSSASTKGSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSW 183
 QY 188 NSGALTSVHTFPVAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKKAEPK 247
 DB 184 NSGALTSVHTFPVAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKKAEPK 243
 QY 248 SCOKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDDEVFENNY 307
 DB 244 SCOKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDDEVFENNY 303
 QY 308 VDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISK 367
 DB 304 VDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISK 363

QY 368 AKQPREPOVYTLPSRDELTKNQVSLTCLVKGPYPSDIAVEHESNQCQPNNTKTPPV 427
 DB 364 AKQPREPOVYTLPSRDELTKNQVSLTCLVKGPYPSDIAVEHESNQCQPNNTKTPPV 423
 QY 428 DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
 DB 424 DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 472

RESULT 11

AAB26884
 ID AAB26884 standard; Protein; 462 AA.

XX AC AAB26884;

XX DT 01-FEB-2001. (first entry)

XX DE Human immunoglobulin heavy chain amino acid sequence.

XX KW Monoclonal antibody; immunoglobulin heavy chain; human.

XX OS Homo sapiens.

XX PN WC200058499-A1.

XX PD 05-OCT-2000.

XX PF 30-MAR-2000; 2000WO-JP02022.

XX PR 30-MAR-1999; 99JP-0087929.

XX PA (NIBS) JAPAN TOBACCO INC.

XX PA (ABGE-) ABGENIX INC.

XX PI Kusunoki C, Fukushima A;

XX DR WPI; 2000-611721/58.

XX DR N-PSDB; AAA09695.

XX PT Transformation of a hybridoma with a gene encoding an immunoglobulin
 heavy chain polypeptide for enhanced production of monoclonal antibody

XX PS Example 2; Page 40-43; 48pp; Japanese.

XX CC This invention relates to a method for the production of a monoclonal
 antibody. The antibody is produced by inserting a gene encoding an
 immunoglobulin heavy chain polypeptide into cells which produce a
 monoclonal antibody recognizing the immunoglobulin, and culturing the
 transformant to express the antibody. The invention also includes
 monoclonal antibody-expressing cells transformed by the method; and
 transgenic non-human animals containing the cells and expressing a human
 antibody. The method results in the enhanced expression of a monoclonal
 antibody for diagnostic and therapeutic use. The present sequence
 represents a human immunoglobulin heavy chain amino acid sequence, the
 cDNA encoding the protein is used in an example of the method of the
 invention.

XX SQ Sequence 462 AA;

Query Match 82.7%; Score 2131; DB 21; Length 462;
 Best Local Similarity 85.4%; Pred. No. 6e-120;
 Matches 409; Conservative 18; Mismatches 32; Indels 20; Gaps 6;

QY 1 MKHLWFFLLVAAPRWLVLSQVQLQKGGGLLPSETLSRTCTVSGGSGISGYVYWTWIRQ 60

DB 1 MKHLWFFLLVAAPRWLVLSQVQLQKGGGLLPSETLSRTCTVSGGSGISGYVYWTWIRQ 59

QY 61 PGKLEWIGHYICNGATTNYPNLSKSRVTISKDTSKNOFFFLNLSVTDADTAVYYCARGP 120

DB 60 PGKLEWIGHYICNGATTNYPNLSKSRVTISKDTSKNOFFFLNLSVTDADTAVYYCAR-- 116

QY 121 RPCTTICVGGWV---DWGPGDGLTVSSASTKGSVFLAPSSKSTSGGTAALGCLVKD 177

CC The present sequence is useful in the diagnosis, treatment and
 CC prevention of disorders associated with the immune system and
 CC cell proliferation.

XX SQ Sequence 470 AA;

Query Match 87.8%; Score 2262; DB 21; Length 470;

Best Local Similarity 90.4%; Pred. No. 8.7e-128;

Matches 433; Conservative 11; Mismatches 23; Indels 12; Gaps 5;

QY 1 MKHLWFFLLVAAPRWLSQVLOQWEGELQPSSETLSRTCVVSGSISGYVYWTWIRQ 60
 DB 1 MKHLWFFLLVAAPRWLSQVLOQWEGELQPSSETLSRTCVVSGSISGYVYWTWIRQ 59
 QY 61 PGRGLEWIGHYNGGATTNNYNSLKRVTISKDTSKNQFFLNLNSVTDADTAVYYCAR 120
 DB 60 PGRGLEWIGHYNGGATTNNYNSLKRVTISKDTSKNQFFLNLNSVTDADTAVYYCAR-P 117
 QY 121 RPDCTTICYGWVDVW---GPGDLVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKD 177
 DB 118 PPNATT-----TTVMTSGAKGALVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKD 171
 QY 178 YFPEPVTVSNMGALTSVGHVTPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHRKPSN 237
 DB 172 YFPEPVTVSNMGALTSVGHVTPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHRKPSN 231
 QY 238 TKVDKKAEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSH 297
 DB 232 TKVDKKAEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSH 291
 QY 298 EDEVEFKNVYVDGVEVHNATKPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 357
 DB 292 EDEVEFKNVYVDGVEVHNATKPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 351
 QY 358 PAPEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 417
 DB 352 PAPEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 411
 QY 418 NNYKTPPVLDSDGSPFLYSKLTVDKSRWQQGNVFPSCSVNHEALHNHYTQKSLSLSPGK 476
 DB 412 NNYKTPPVLDSDGSPFLYSKLTVDKSRWQQGNVFPSCSVNHEALHNHYTQKSLSLSPGK 470

RESULT 9

AAAR93553
 ID AAR93553 standard; Protein; 475 AA.

XX AC AAR93553;

XX DT 20-AUG-1996 (first entry)

XX DE Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.

XX KW Polymerase chain reaction; primer; amplifiy; PCR; light chain; MAB;
 XX 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 XX FT Peptide 1..19
 XX FT Protein /note= "Signal peptide"
 XX FT /note= "Mature heavy chain"

XX PN JP08038178-A.

XX PD 13-FEB-1996.

XX PF 20-FEB-1995; 95JP-0030742.

XX PR 18-FEB-1994; 94JP-0021628.

XX PA (NIN) NISSHINO IND INC.

PA (TANA/) TANAKA H.

XX MPI; 1996-154852/16.

XX N-PSDB; AAT18059.

XX Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -
 PT produced by primer amplification, used in the diagnosis of hCMV
 PT infection

XX Claim 4; Page 16-18; 22pp; Japanese.

XX The sequences given in AAR93553-54 represent the heavy and light chains
 CC respectively of a monoclonal antibody against a 65 kD antigen of human
 CC cytomegalovirus (hCMV). The DNA s encoding these sequences were
 CC amplified using the sequences given in AAT18040-58. The monoclonal
 CC antibody may be used in the diagnosis of hCMV.

XX SQ Sequence 475 AA;

Query Match 86.6%; Score 2230.5; DB 17; Length 475;

Best Local Similarity 89.7%; Pred. No. 6.8e-126;

Matches 428; Conservative 11; Mismatches 35; Indels 3; Gaps 3;

QY 1 MKHLWFFLLVAAPRWLSQVLOQWEGELQPSSETLSRTCVVSGSISGYVYWTWIRQ 59

DB 1 MKHLWFFLLVAAPRWLSQVLOQWEGELQPSSETLSRTCVVSGSISRSSYSWGCIQ 60

QY 60 TPGRGLEWIGHYNGGATTNNYNSLKRVTISKDTSKNQFFLNLNSVTDADTAVYYCAR 119

DB 61 PGRGLEWIGHYNGGATTNNYNSLKRVTISKDTSKNQFFLNLNSVTDADTAVYYCAR - 118

QY 120 PRPDCTTICYGWVDVWPGDLVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYF 179

DB 119 TSPQYDILLTSGPSPYMGQGTLTVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYF 178

QY 180 PEPVTVSNMGALTSVGHVTPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHRKPSNTK 239

DB 179 PEPVTVSNMGALTSVGHVTPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHRKPSNTK 238

QY 240 VDKKAEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHED 299

DB 239 VDKKAEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHED 298

QY 300 PSEVKNVYVDGVEVHNATKPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359

DB 299 PSEVKNVYVDGVEVHNATKPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 358

QY 360 PIEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419

DB 359 PIEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 418

QY 420 YKTPPVLDSDGSPFLYSKLTVDKSRWQQGNVFPSCSVNHEALHNHYTQKSLSLSPGK 476

DB 419 YKTPPVLDSDGSPFLYSKLTVDKSRWQQGNVFPSCSVNHEALHNHYTQKSLSLSPGK 475

RESULT 10

AAAR93166

ID AAR93166 standard; Protein; 472 AA.

XX AC AAR93166;

XX DT 30-OCT-1996 (first entry)

XX DE Anti-rhesus D recombinant antibody D7C2 heavy chain.

XX KW Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;
 XX rhesus positive; rhesus negative; haemolysis; gamma 1 heavy chain;
 XX variable region; insect host cell; baculovirus; recombinant production.

XX OS Homo sapiens.

XX OS Synthetic.


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PS Claim 1; Column 53-56; 54pp; English.
XX
CC The present invention provides the coding and protein sequences for a
CC number of human immune system associated proteins (HISAPs). These can be
CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, anorexia, multiple sclerosis, myasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
SQ Sequence 473 AA;
Query Match 88.4%; Score 2277.5; DB 22; Length 473;
Best Local Similarity 90.8%; Pred. No. 1e-128;
Matches 434; Conservative 16; Mismatches 21; Indels 7; Gaps 4;
QY 1 MKHLFFLLVAAPRWLSQVQLQWGGELQPSLTLSLRTCTVSGGSI-SGYVYWTIRQ 59
Db 1 MKHLFFLLVAAPRWLSQVQLQWGGELQPSLTLSLRTCTVSGGSI-SGYVYWTIRQ 60
QY 60 TPGRLGLEWIGHYNGATTNPNPSLKSRVTISKDPSKNOFFLNLSVTDADTAVYYCARG 119
Db 61 PPGKLEWIGHYIYSGSTL-INPSLKSRVTISVDTSKNOFSLKSSVTAADTAVYYCAR- 118
QY 120 PRPDCTTICYGW-VDMVGPGLVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDY 178
Db 119 ---DVGRLGGNYGMDVWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDY 175
QY 179 PPEPVTVSNAGSLTSGVHTPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNT 238
Db 176 PPEPVTVSNAGSLTSGVHTPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNT 235
QY 239 KVDKAEKPKSCDKTHCTCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSH 298
Db 236 KVDKAEKPKSCDKTHCTCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSH 295
QY 299 DPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 358
Db 296 DPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 355
QY 359 APIETISKAGQREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPEN 418
Db 356 APIETISKAGQREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPEN 415
QY 419 NYKTPPVLDSDGSFFLYSKLTVDKSRQQQGNVFCSCVMHEALHNNHVTQKLSLSLSPGK 476
Db 416 NYKTPPVLDSDGSFFLYSKLTVDKSRQQQGNVFCSCVMHEALHNNHVTQKLSLSLSPGK 473
RESULT 8
AA44721
ID AAY44721 standard; Protein; 470 AA.
XX
AC AA44721;
XX
DT 25-APR-2000 (first entry)
XX
DE Human immune system molecule, ISMO-2.
XX
KW Human; immune system molecule; ISMO-2; Incyte clone 2849752; diagnosis;
KW treatment; prevention; cell proliferation; immune system disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Signal_peptide
FT Protein 20..470
FT Modified-site /label= Mature_ISMO-2
FT Modified-site 120
FT Modified-site /note= "N-glycosylated"
FT Modified-site 320

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FT Modified-site 105
FT Modified-site /note= "N-glycosylated"
FT Modified-site 232
FT Modified-site /note= "Casein kinase II phosphorylation site"
FT Modified-site 290
FT Modified-site /note= "Casein kinase II phosphorylation site"
FT Modified-site 377
FT Modified-site /note= "Casein kinase II phosphorylation site"
FT Modified-site 47
FT Modified-site /note= "Casein kinase II phosphorylation site"
FT Modified-site 81
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT Modified-site 92
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT Modified-site 98
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT Modified-site 142
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT Modified-site 154
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT Modified-site 322
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT Modified-site 347
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT Modified-site 460
FT Modified-site /note= "Protein kinase C phosphorylation site"
FT Modified-site 69
FT Modified-site /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 319
FT Modified-site /note= "Tyrosine kinase phosphorylation site"
FT Region 387..409
FT Region /note= "conserved Ig/MHC protein block"
FT Region 446..463
FT Domain /note= "conserved Ig/MHC protein block"
FT Domain 34..116
FT Domain /note= "shows similarity to Ig superfamily protein domain"
FT Domain 160..225
FT Domain /note= "shows similarity to Ig superfamily protein domain"
FT Domain 383..450
FT Domain /note= "shows similarity to Ig superfamily protein domain"
XX WO200000608-A2.
XX
XX 06-JAN-2000.
XX
XX 21-JUN-1999; 99WO-US13995.
XX
XX 30-JUN-1998; 98US-0107223.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Lal P, Tang YT, Corley NC, Gorgone G, Guegler KJ, Patterson C;
XX Baughn MR;
XX WPI; 2000-170916/15.
XX N-PSDB; AAZ50012.
XX
XX Immune system molecules used in the diagnosis, treatment and prevention
XX of disorders associated with the immune system and cell proliferation
XX
XX Claim 1; Pages 60-61; 69pp; English.
XX
XX The present sequence is an immune system molecule.
XX ISMO-2 from an incyte clone 2849752 isolated from the human breast
XX tumour cDNA library (BRSTRUT13). This sequence is expressed in several
XX libraries, generally those associated with cancer, cell
XX proliferation, immune response or trauma. It shows homology to
XX vertebrate immunoglobulin gamma heavy-chain.

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QY 361 IBKTSKAGQPREQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 Db 361 IBKTSKAGQPREQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 QY 421 KTTTPVLDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 476
 Db 421 KTTTPVLDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 476

RESULT 6
 AAU11646
 ID AAU11646 standard; Protein; 476 AA.
 XX
 AC AAU11646;
 DT 12-MAR-2002 (first entry)
 XX
 DE Protein sequence of primatised form of the heavy chain of 16C10 antibody.
 KW Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
 KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
 KW graft-vs-host disease; immunosuppression; organ rejection;
 KW interleukin-2; IL-2; mutant; mutein.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Macaca sp.
 OS Synthetic.
 XX
 PN WO200189567-A1.
 XX
 PD 29-NOV-2001.
 XX
 PF 22-MAY-2001; 2001WO-US16364.
 XX
 PR 22-MAY-2000; 2000US-0576424.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 XX Anderson DR, Hanna N, Brams P;
 XX WPI; 2002-089895/12.
 XX N-PSDB; AAS17247.
 XX
 XX Use of monoclonal antibody which specifically binds to B7.1 antigen
 CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
 treating cancer, graft-vs-host disease and autoimmune disease such as
 allergy -
 XX
 XX Example 8; Fig 5b; 89pp; English.
 PS
 CC The present invention relates to a new use of a monoclonal antibody
 which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
 (CD86) for inducing the apoptosis of B7+ cells. The invention is
 useful for treating diseases such as B cell cancer, lymphoma, a
 cancer where B cells promote the growth and/or metastasis of tumours,
 B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
 idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
 type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
 anaemia, inflammatory bile disease, allergy, multiple sclerosis
 or graft-vs-host disease. The antibody is useful for immunosuppression
 in a human or animal and for treating or preventing resistance to or
 rejection of transplanted organ or tissue for treating proliferative
 and hyperproliferative diseases, for treating reversible obstructive
 airways disease, intestinal inflammations and allergies e.g. Crohn's
 disease and ulcerative colitis, food-related allergies e.g. migraine,
 rhinitis and eczema, and other types of allergies. The present protein
 sequence represents the heavy chain of 16C10, a primatised antibody
 used in the invention to induce apoptosis and inhibit production of
 interleukin-2 (IL-2).
 XX
 XX Sequence 476 AA;

Query Match 89.68; Score 2309; DB 23; Length 476;
 Best Local Similarity 91.2%; Pred. No. 1.4e-130;
 Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MKHLWFFLLVAAPRWLVSQVQLQWGEGLLPQSETLSRTCTVSVSGSISGYVYTWIRQT 60
 Db 1 MKHLWFFLLVAAPRWLVSQVQLQWGEGLLPQSETLSRTCTVSVSGSISGYVYTWIRQT 60
 QY 61 PORGLEWIGHYGNATNYPNPSLKSRVTISKDTSKNOFFNLNSVTDATATYTCARGP 120
 Db 61 PKGLEWIGSFYSSGNTYNNPSLKSVQTTSTDTSKNQPSLKLNSMTAADTAVYVCVDR 120
 QY 121 RPDCTTICYGWVDWVGPDLVTVSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFP 180
 Db 121 LFSVVGMVYNNWFDWVGPGVLTVTSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFP 180
 QY 181 EPTVTVMNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKV 240
 Db 181 EPTVTVMNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKV 240
 QY 241 DKKAEPKSCDKHTCCPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
 Db 241 DKKAEPKSCDKHTCCPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
 QY 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLTQHDWLNKGKEYCKVSNKALPAP 360
 Db 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLTQHDWLNKGKEYCKVSNKALPAP 360
 QY 361 IEKTSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 Db 361 IEKTSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 QY 421 KTTTPVLDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 476
 Db 421 KTTTPVLDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 476

RESULT 7
 AAB36206
 ID AAB36206 standard; protein; 473 AA.
 XX
 AC AAB36206;
 XX
 DT 15-FEB-2001 (first entry)
 XX
 DE Human immune system associated protein HisAP-4.
 XX
 KW Human; immune system associated protein; HisAP-4; immune disorder;
 infection; autoimmune disease; cancer.
 XX
 OS Homo sapiens.
 XX
 PN US6135941-A.
 XX
 PD 24-OCT-2000.
 XX
 PF 27-MAR-1998; 98US-0049672.
 XX
 PR 27-MAR-1998; 98US-0049672.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
 Hillman J, Au-Young J;
 XX
 XX WPI; 2001-030926/04.
 DR N-PSDB; AAC66522.
 DR
 XX New human immune system associated proteins (HisAP) and polynucleotides
 encoding the HisAP, useful for diagnosing, treating or preventing
 immune or cell proliferative disorders or infections -
 PT
 PT

```

XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT useful for treating autoimmune disease or graft-versus-host disease
XX
XX Claim 14; Fig 10B; 8lpp; English.
XX
CC 2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised
CC forms of the light and heavy chains of cynomolgus monkey anti-human
CC B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and
CC heavy variable genes (see also AAT62512 and AAT62513) are inserted into
CC an expression vector (pref. NEO5PLA) which contains human light and
CC heavy chain constant genes to allow prodn. of the primatised
CC antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
CC antibodies have also been produced (see also AAW01817-20). The
CC primatised antibodies inhibit the B7:CD28 pathway, making them
CC useful immunosuppressants for the treatment of autoimmune disorders
CC and graft-versus-host disease.
XX
XX Sequence 476 AA;
XX
Query Match 89.6%; Score 2309; DB 18; Length 476;
Best Local Similarity 91.2%; Pred. No. 1.4e-130;
Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;
XX
Qy 1 MKHLWFFLLVAAPRWLSQVQLQWGGELLPQSETLSRTCTVSGSGISGYYYWTWIRQT 60
Db 1 MKHLWFFLLVAAPRWLSQVQLQWGGELLPQSETLSLTCAVSGSGISGYGWMIRQP 60
Qy 61 PGRGLEWIGHYNGATTNNPNSLKSRVTISKDTSKNQFFLNLSVTDADTAVYYCARGP 120
Db 61 PGRGLEWIGSFYSSGNTYNNPSLKSQVTISTDTSKNQFSLKLSMTAADTAVYYCVRDR 120
Qy 121 RPDCTTICVGGWVDVWPGDLVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYEP 180
Db 121 LFSVGVWYNNWDFVWPGVLTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFP 180
Qy 181 EPTVTSWNSGALTSQVHTFPFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKV 240
Db 181 EPTVTSWNSGALTSQVHTFPFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKV 240
Qy 241 DKKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDP 300
Db 241 DKKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDP 300
Qy 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
Db 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
Qy 361 IEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
Db 361 IEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
Qy 421 KTTTPVLSDGSGFFLYSKLTVDKSRWQQGNVPCSCVMHEALHNYHTQKSLSLSPGK 476
Db 421 KTTTPVLSDGSGFFLYSKLTVDKSRWQQGNVPCSCVMHEALHNYHTQKSLSLSPGK 476
XX
RESULT 5
AAW63765
ID AAW63765 standard; Protein; 476 AA.
XX
XX AAW63765;
XX
DT 29-SEP-1998 (first entry)
XX
DE Macaque primatised 16C10 heavy chain protein.
XX
KW Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW T cell proliferation.
XX

```

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OS Macaca fascicularis.
XX
PN WO9819706-A1.
XX
PD 14-MAY-1998.
XX
PF 29-OCT-1997; 97WO-US19906.
XX
PR 08-NOV-1996; 96US-0746361.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
XX Anderson DR, Brams P, Hanna N;
DR WPI: 1998-286601/25.
DR N-PSDB; AAV35489.
XX
PT New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT inhibiting binding to CD28 - useful as specific immunosuppressants
PT for treating diseases that involve interactions between T and B
PT cells, e.g. graft rejection or tumours
XX
PS Example 7; Fig 5b; 87pp; English.
XX
CC This sequence represents a primatised form of the antibody 16C10 heavy
CC chain from macaque. This sequence is used in a method which studies new
CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC Mab's are specific immunosuppressants for treatment of diseases involving
CC T cell/B cell interactions, particularly autoimmune disease, specifically
CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC host diseases, B cell lymphoma, infections (including by human immune
CC deficiency virus) or inflammatory disease and tumours. Optionally the
CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
CC also be used as imaging agents and as vaccines or immunogens to develop
CC anti-idiotype reagents. Mab's are optionally combined with other proteins
CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC production of interleukin-2 (IL-2), T cell proliferation and
CC antigen-specific immunoglobulin G (IgG) responses.
XX
SQ Sequence 476 AA;
XX
Query Match 89.6%; Score 2309; DB 19; Length 476;
Best Local Similarity 91.2%; Pred. No. 1.4e-130;
Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;
XX
Qy 1 MKHLWFFLLVAAPRWLSQVQLQWGGELLPQSETLSRTCTVSGSGISGYYYWTWIRQT 60
Db 1 MKHLWFFLLVAAPRWLSQVQLQWGGELLPQSETLSLTCAVSGSGISGYGWMIRQP 60
Qy 61 PGRGLEWIGHYNGATTNNPNSLKSRVTISKDTSKNQFFLNLSVTDADTAVYYCARGP 120
Db 61 PGRGLEWIGSFYSSGNTYNNPSLKSQVTISTDTSKNQFSLKLSMTAADTAVYYCVRDR 120
Qy 121 RPDCTTICVGGWVDVWPGDLVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFP 180
Db 121 LFSVGVWYNNWDFVWPGVLTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFP 180
Qy 181 EPTVTSWNSGALTSQVHTFPFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKV 240
Db 181 EPTVTSWNSGALTSQVHTFPFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKV 240
Qy 241 DKKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDP 300
Db 241 DKKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDP 300
Qy 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
Db 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

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QY 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 DB 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 QY 421 KTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK 476
 DB 421 KTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK 476

RESULT 3
 AAU11539
 ID AAU11539 standard; Protein; 476 AA.
 XX
 AC AAU11539;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Protein sequence of primatised form of the heavy chain of 7C10 antibody.
 XX
 KW Human; macaque monkey; light chain; primatised antibody; 7C10 antibody;
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
 KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
 KW graft-vs-host disease; immunosuppression; organ rejection;
 KW interleukin-2; IL-2; mutant; mutein.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Macaca sp.
 OS Synthetic.
 XX
 PN W0200189567-A1.
 XX
 PD 29-NOV-2001.
 XX
 PF 22-MAY-2001; 2001WO-US16364.
 XX
 PR 22-MAY-2000; 2000US-0576424.
 XX
 XX (IDEC-) IDEC PHARM CORP.
 XX
 XX Anderson DR, Hanna N, Brama P;
 XX
 DR WPI; 2002-089895/12.
 DR N-PSDB; AAS17243.
 XX
 XX Use of monoclonal antibody which specifically binds to B7.1 antigen
 PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, as
 PT treating cancer, graft-vs-host disease and autoimmune disease such as
 PT allergy -
 XX
 PS Example 8; Fig 3b; 89pp; English.
 XX
 CC The present invention relates to a new use of a monoclonal antibody
 CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
 CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
 CC useful for treating diseases such as B cell cancer, lymphoma, a
 CC cancer where B cells promote the growth and/or metastasis of tumours,
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
 CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
 CC or graft-vs-host disease. The antibody is useful for immunosuppression
 CC in a human or animal and for treating or preventing resistance to or
 CC rejection of transplanted organ or tissue for treating proliferative
 CC and hyperproliferative diseases, for treating reversible obstructive
 CC airways disease, intestinal inflammations and allergies e.g. Crohn's
 CC disease and ulcerative colitis, food-related allergies e.g. migraine,
 CC rhinitis and eczema, and other types of allergies. The present protein
 CC sequence represents the heavy chain of 7C10, a primatised antibody
 CC used in the invention to induce apoptosis and inhibit production of
 CC interleukin-2 (IL-2).
 XX

SQ Sequence 476 AA;
 Query Match 100.0%; Score 2577; DB 23; Length 476;
 Best Local Similarity 100.0%; Pred. No. 1.2e-146;
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKHLWFFLLVAAPRWLSQVKLQWGEGLLPSETLSRTCTCVSGSGISGYYWTWIRQT 60
 DB 1 MKHLWFFLLVAAPRWLSQVKLQWGEGLLPSETLSRTCTCVSGSGISGYYWTWIRQT 60
 QY 61 PGRGLEWIGHIYNGATTNYPNLSKSRVTISKDTSKNOFFLNLSVTDADTAVYTCARGP 120
 DB 61 PGRGLEWIGHIYNGATTNYPNLSKSRVTISKDTSKNOFFLNLSVTDADTAVYTCARGP 120
 QY 121 RPDCTTICYGHWVDVWPGDLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
 DB 121 RPDCTTICYGHWVDVWPGDLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
 QY 181 EPTVTSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHPSTNTKV 240
 DB 181 EPTVTSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHPSTNTKV 240
 QY 241 DKKAEPKCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
 DB 241 DKKAEPKCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
 QY 301 EVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLDHQLNGKEYCKVKSNKALPAP 360
 DB 301 EVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLDHQLNGKEYCKVKSNKALPAP 360
 QY 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 DB 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 QY 421 KTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK 476
 DB 421 KTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK 476

RESULT 4

AAW01822
 ID AAW01822 standard; Protein; 476 AA.
 XX
 AC AAW01822;
 XX
 DT 25-MAY-1997 (first entry)
 XX
 DE Primatised anti-human B7.1 antigen antibody 16C10 heavy chain.
 XX
 KW Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
 KW primatised antibody; B7 antigen; CD28; immunosuppressive;
 KW autoimmune disease; idiopathic thrombocytopenia purpura;
 KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
 KW type 1 diabetes mellitus; graft versus host disease;
 KW hetero-hybridoma; transfectoma.
 XX
 OS Chimeric Macaca cynomolgus;
 OS Chimeric Homo sapiens.
 XX
 PN W09640878-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US10053.
 XX
 PR 07-JUN-1995; 95US-0487550.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Anderson DR, Brama P, Hanna N, Shestowsky WS;
 XX
 DR WPI; 1997-108638/10.
 DR N-PSDB; AAT62513.

DR N-PSDB; AAT62510.
 XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
 PT useful for treating autoimmune disease or graft-versus-host disease
 XX
 PS Claim 6; Fig 8B; 81pp; English.
 XX
 CC 2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised
 CC forms of the light and heavy chains of cynomolgus monkey anti-human
 CC B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy
 CC variable genes (see also AAT62509 and AAT62510) are inserted into
 CC an expression vector (pref. NEOSPLA) which contains human light and
 CC heavy chain constant region genes to allow prodn. of the primatised
 CC antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1
 CC antibodies have also been produced (see also AAW01819-22). The
 CC primatised antibodies inhibit the B7:CD28 pathway, making them
 CC useful immunosuppressants for the treatment of autoimmune disorders
 CC and graft-versus-host disease.
 XX
 SQ Sequence 476 AA;
 Query Match 100.0%; Score 2577; DB 18; Length 476;
 Best Local Similarity 100.0%; Pred. No. 1.2e-146;
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKHLWFFLLVAAAPRWVLSQVKLQOMGEGLLQPSSETLSRTCVVSGSISGYVYWTWIRQT 60
 Db 1 MKHLWFFLLVAAAPRWVLSQVKLQOMGEGLLQPSSETLSRTCVVSGSISGYVYWTWIRQT 60
 Qy 61 PGRLEWIGHYGNAGATTNNPSLKSRTVTSKDTSKNOFFNLNSVTDADTAVYVCARGP 120
 Db 61 PGRLEWIGHYGNAGATTNNPSLKSRTVTSKDTSKNOFFNLNSVTDADTAVYVCARGP 120
 Qy 121 RPDCTTCYCGWVDVWPGDLVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFP 180
 Db 121 RPDCTTCYCGWVDVWPGDLVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFP 180
 Qy 181 EPVTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNKTKV 240
 Db 181 EPVTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNKTKV 240
 Qy 241 DKKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKDRLMIISRTPEVTCVVDVDSHPD 300
 Db 241 DKKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKDRLMIISRTPEVTCVVDVDSHPD 300
 Qy 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
 Db 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
 Qy 361 IEKTSKAGQPREPQVYTLPPSDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 Db 361 IEKTSKAGQPREPQVYTLPPSDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
 Qy 421 KTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCFVSNMHEALHNHYTQKSLSLSPGK 476
 Db 421 KTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCFVSNMHEALHNHYTQKSLSLSPGK 476
 RESULT 2
 AAW63761
 ID AAW63761 standard; Protein; 476 AA.
 XX
 AC AAW63761;
 XX
 DT 29-SEP-1998 (first entry)
 XX
 DE Macaque primatised 7C10 heavy chain DNA.
 DE
 KW Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
 KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
 KW T cell proliferation; ss.

XX OS Macaca fascicularis.
 XX WO9819706-A1.
 XX 14-MAY-1998.
 XX 29-OCT-1997; 97WO-US19906.
 XX 08-NOV-1996; 96US-0746361.
 XX (IDEC-) IDEC PHARM CORP.
 XX Anderson DR, Brams P, Hanna N;
 WPI; 1998-286601/25.
 DR N-PSDB; AAV35485.
 XX
 PT New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 PT inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 PT cells, e.g. graft rejection or tumours
 PT
 PS Example 7; Fig 3b; 87pp; English.
 XX
 CC This sequence represents a primatised form of the antibody 7C10 heavy
 CC chain from macaque. This sequence is used in a method which studies new
 CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC Mab's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 CC host diseases, B cell lymphoma, infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop
 CC anti-idiotypic reagents. Mab's are optionally combined with other proteins
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.
 XX
 SQ Sequence 476 AA;
 Query Match 100.0%; Score 2577; DB 19; Length 476;
 Best Local Similarity 100.0%; Pred. No. 1.2e-146;
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKHLWFFLLVAAAPRWVLSQVKLQOMGEGLLQPSSETLSRTCVVSGSISGYVYWTWIRQT 60
 Db 1 MKHLWFFLLVAAAPRWVLSQVKLQOMGEGLLQPSSETLSRTCVVSGSISGYVYWTWIRQT 60
 Qy 61 PGRLEWIGHYGNAGATTNNPSLKSRTVTSKDTSKNOFFNLNSVTDADTAVYVCARGP 120
 Db 61 PGRLEWIGHYGNAGATTNNPSLKSRTVTSKDTSKNOFFNLNSVTDADTAVYVCARGP 120
 Qy 121 RPDCTTCYCGWVDVWPGDLVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFP 180
 Db 121 RPDCTTCYCGWVDVWPGDLVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFP 180
 Qy 181 EPVTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNKTKV 240
 Db 181 EPVTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNKTKV 240
 Qy 241 DKKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKDRLMIISRTPEVTCVVDVDSHPD 300
 Db 241 DKKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKDRLMIISRTPEVTCVVDVDSHPD 300
 Qy 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
 Db 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 48.9575 Seconds
(without alignments)
1295.559 Million cell updates/sec

Title: US-09-758-173-4

Perfect score: 2577

Sequence: 1 MKHLWFLVLAAPRWLSQ.....MHEALHHYQKSLSPGK 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2577	100.0	476	18 AAW01818	Primates anti-hu
2	2577	100.0	476	19 AAW63761	Macaque primatized
3	2577	100.0	476	23 AAU11539	Protein sequence o
4	2309	89.6	476	18 AAW01822	Primates anti-hu
5	2309	89.6	476	19 AAW63765	Macaque primatized
6	2309	89.6	476	23 AAU11646	Protein sequence o
7	2277.5	88.4	473	22 AAB36206	Human immune syste
8	2262	87.8	470	21 AAY44721	Human immune syste
9	2230.5	86.6	475	17 AAR93553	Monoclonal antibod
10	2223	86.3	472	17 AAR93166	Anti-rhesus D reco

11	2131	82.7	21	AAB26884	Human immunoglobul
12	2122	82.3	470	13 AAR22757	Reshaped CAMPATH-1
13	2112.5	82.0	467	18 AAW14927	Human gamma-4E he
14	2111.5	81.9	467	18 AAW14925	Human gamma-4 heav
15	2107.5	81.8	475	22 AAG63640	Amino acid sequenc
16	2104.5	81.7	467	18 AAW14926	Human gamma-4E hea
17	2104.5	81.7	581	22 AAB81972	Reaggliside GD2 ep
18	2103.5	81.6	467	13 AAR22759	Reshaped CD4 antib
19	2100.5	81.5	467	13 AAR22758	Reshaped CD4 antib
20	2100	81.5	451	20 AAW95659	Mus musculus anti-
21	2100	81.5	451	20 AAW95661	Mus musculus anti-
22	2100	81.5	451	21 AAY85201	Light chain amino
23	2100	81.5	451	22 AAB74088	Anti-IgE antibody,
24	2100	81.5	451	22 AAB76948	Full length heavy,
25	2100	81.5	451	22 AAB76950	Full length heavy,
26	2092	81.2	451	20 AAY50031	Human E27 anti-IgE
27	2092	81.2	451	20 AAW95663	Mus musculus anti-
28	2092	81.2	451	21 AAB07473	Amino acid sequenc
29	2092	81.2	451	22 AAB74212	E27 anti-IgE antib
30	2092	81.2	451	22 AAB76952	Full length heavy
31	2091.5	81.2	446	17 AAW05829	Humanised 1D10 ant
32	2079.5	80.7	475	18 AAW11639	Human anti-RSV mon
33	2077	80.6	470	21 AAU77289	Protein #2 in inve
34	2073	80.4	478	19 AAW63763	Macaque primatized
35	2073	80.4	478	23 AAU11644	Protein sequence o
36	2069.5	80.3	481	13 AAR24442	Sequence of anti-bo
37	2069	80.3	453	14 AAR33311	Humanised MaEl1 Ve
38	2069	80.3	453	21 AAY85199	Heavy chain amino
39	2067	80.2	478	18 AAW01820	Primates anti-hu
40	2061.5	80.0	452	20 AAY29458	Recombinant immuno
41	2061.5	80.0	452	21 AAB30322	Humanised anti-IL-
42	2061.5	80.0	452	21 AAY77766	Humanised anti-IL-
43	2057.5	79.8	477	22 AAB42288	Human novel protei
44	2057	79.8	476	22 AAB49243	Chimeric 4H6 anti-
45	2053	79.7	470	21 AAB08026	A dimeric anti-CD2

ALIGNMENTS

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RESULT 1
AAW01818
ID AAW01818 standard; Protein; 476 AA.
AC
XX AAW01818;
XX
XX
DT 25-MAY-1997 (first entry)
DE Primatised anti-human B7.1 antigen antibody 7C10 heavy chain.
XX
KW Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW primatised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma.
XX
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX
FN WO9640878-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US10053.
XX
PR 07-JUN-1995; 95US-0487550.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX WPI; 1997-108638/10.

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Qy	20	QVKLOQWEGELLQPSSETLSRTCVVSGSGSISGYIYWTWIRQTPGRGLEWIGHIYNGATTN	79
Db	1	EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASITYDG-STN	59
Qy	80	YNPSLKSRVTTISKDTSKNQFFLNLSNVTADTAVYYCARGPRPDCTTICYGWS-VDVWGP	138
Db	60	YADSVKGRFTISRDSDSKNTFYLQMNSLRRAEDTAVYYCARGSH-----YFGHWHFAVWVGQ	113
Qy	139	GDLVTVSSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPFTVSWNSGALTSGV	196
Db	114	GTLLTVSSASTKGKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPFTVSWNSGALTSGV	173
Qy	197	HTFPAVLSSGLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCP	256
Db	174	HTFPAVLSSGLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCP	233
Qy	257	PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA	316
Db	234	PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA	293
Qy	317	KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ	376
Db	294	KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ	353
Qy	377	VYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPTPLDSDGSPFLY	436
Db	354	VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPTPLDSDGSPFLY	413
Qy	437	SKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK	476
Db	414	SKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK	453

Search completed: March 29, 2003, 09:38:37
Job time : 19.2478 secs

SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-948-429B-8

Query Match 80.4%; Score 2073; DB 9; Length 478;
Best Local Similarity 83.9%; Pred. No. 1.7e-106;
Matches 396; Conservative 21; Mismatches 51; Indels 4; Gaps 3;

QY 8 LLLVAAPRWLSOVKLOQWEGELLPSETLSRTCVVSGSISGYIYWTWIRTPGRGLEW 67
DB 8 LFLVAVATRVQCEVQLVGGGLVQPGSLRVSCAVSGFTSDHYMY-WFRQAPGKGPW 66
QY 68 IGHYIG--NGATTNPNLSKRVITISKDTSKNOFFNLNLSVTDADTAVYYCARGPRDCT 125
DB 67 VGFIRKPNPGGTTTEYAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYYCTTSVISHCR 126
QY 126 -TICYGGVDMVMPGDLVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVT 184
DB 127 GGVYGGYEFWQOGALVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVT 186
QY 185 VSNNSGALTSVGHVTPPAVLQSSGLSLSVWTVVPSSSLGTQTYICNVNPKPSNTKVDKKA 244
DB 187 VSNNSGALTSVGHVTPPAVLQSSGLSLSVWTVVPSSSLGTQTYICNVNPKPSNTKVDKKA 246
QY 245 EPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 304
DB 247 EPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 306
QY 305 NMYVDGVEVHNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 364
DB 307 NMYVDGVEVHNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 366
QY 365 ISKAKGQPREPOVYITPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 424
DB 367 ISKAKGQPREPOVYITPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 426
QY 425 PVLDSGGSFLLYSLKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 476
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RESULT 14
US-09-925-179-8
; Sequence 8, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:

; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P07182C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-925-179-8

Query Match 80.3%; Score 2069; DB 9; Length 453;
Best Local Similarity 85.7%; Pred. No. 2.6e-106;
Matches 394; Conservative 19; Mismatches 37; Indels 10; Gaps 4;

QY 20 QVKLQWEGELLPSETLSRTCVVSGSISGYIYWTWIRTPGRGLEWIGHIYNGATTN 79
DB 1 EVQLWESGGGLVQPGSLRVSCAVSGYISITSGYSWNIWIRQAPGKLEWVASITYDG-STN 59
QY 80 YNPGLKSRVTISKDTSKNOFFNLNLSVTDADTAVYYCARGPRDCTTICYGGW-VDVWGP 138
DB 60 YAUDSVKGRFTISRDDSKNTFYLQMSLSRAEDTAVYYCARGSH-----YFGHWHFAVMGQ 113
QY 139 GDLVTVSSAST--KGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSNNSGALTSGV 196
DB 114 GTLVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSNNSGALTSGV 173
QY 197 HTPPAVLQSSGLSLSVWTVVPSSSLGTQTYICNVNPKPSNTKVDKKAEPKSCDKTHTCP 256
DB 174 HTPPAVLQSSGLSLSVWTVVPSSSLGTQTYICNVNPKPSNTKVDKKAEPKSCDKTHTCP 233
QY 257 PCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 316
DB 234 PCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 293
QY 317 KTKPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 376
DB 294 KTKPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 353
QY 377 VYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLY 436
DB 354 VYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLY 413
QY 437 SKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 476
DB 414 SKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 453

RESULT 15

US-09-802-077-8
; Sequence 8, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:

; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P07182C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-802-077-8

Query Match 80.3%; Score 2069; DB 10; Length 453;
Best Local Similarity 85.7%; Pred. No. 2.6e-106;
Matches 394; Conservative 19; Mismatches 37; Indels 10; Gaps 4;

QY 187 WNSGALTSVHTFPVAVLQSSGLYSLSSVTVVTPSSISGTTQTYICNVNHHKPSNTKVDKKAEP 246
DB 186 WNSGALTSVHTFPVAVLQSSGLYSLSSVTVVTPSSISGTTQTYICNVNHHKPSNTKVDKKAEP 245
QY 247 KSCDKHTHTCPCPAPPELLGGPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNW 306
DB 246 KSCDKHTHTCPCPAPPELLGGPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNW 305
QY 307 YDGVVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 366
DB 306 YDGVVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 365
QY 367 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 426
DB 366 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 425
QY 427 LQSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 476
DB 426 LQSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 475

RESULT 12
US-10-124-905-8
; Sequence 8, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-124-905-8

Query Match 80.4%; Score 2073; DB 9; Length 478;
Best Local Similarity 83.9%; Pred. No. 1.7e-106;
Matches 396; Conservative 21; Mismatches 51; Indels 4; Gaps 3;

QY 8 LLLVAAPRWVLSOVKIQWGEGLLPQSETLSRTCVVSGSISGYYTWTWIRQTPRGLEW 67
DB 8 LFLVAVATRVQCEVQLVVEGGLVQPGGLRVSCAVSGFTFSDHNYM - WFRQAPGKGPW 66
QY 68 IGHYIG--NGATTNYPNLSKSRVTISKDTSKNOFFFLNLSVTDADTAVVYCARGRPDC 125
DB 67 VGFIRNPNNGTTEYAAASVADRTTISRDDSKSIAYLQMSLKIETAVVYCTTSYISHCR 126
QY 126 -TTCYCGWVDVWPGDLVTVSSASTKPSVFPPLAPSSTSGTGAALGCLVKDYFPEPVT 184
DB 127 GVCYGGYFFWQGGALVTVSSASTKPSVFPPLAPSSTSGTGAALGCLVKDYFPEPVT 186
QY 185 VSMNSGALTSGVHTFPVAVLQSSGLYSLSSVTVVTPSSISGTTQTYICNVNHHKPSNTKVDKKA 244
DB 187 VSMNSGALTSGVHTFPVAVLQSSGLYSLSSVTVVTPSSISGTTQTYICNVNHHKPSNTKVDKKA 246
QY 245 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 304
DB 247 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 306
QY 305 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 364
DB 307 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 366
QY 365 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 424
DB 367 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 426
QY 425 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 476
DB 427 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 478

RESULT 13
US-09-948-429B-8
; Sequence 8, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:

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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)9 of Table
US-09-925-179-68

Query Match      81.5%; Score 2099; DB 9; Length 451;
Best Local Similarity 86.7%; Pred. No. 6e-108;
Matches 397; Conservative 18; Mismatches 35; Indels 8; Gaps 3;

QY 20 QVKLQWGEGLLOPSETLRTCTCVVSGSISGYVYVWIRQTQGRGLEWIGHYVGNATTN 79
DQ 1 EVQLVESGGGLVPGGSLRLSCAASGYSITSGYSMWIRQAPGKGLEWVASIKYSG-ETK 59
EVLVESGGGLVPGGSLRLSCAASGYSITSGYSMWIRQAPGKGLEWMSITYDG-STN 59
QY 80 YNPSLKSRVTISKDTSKNOFFLNLSVTDADTAVYVCARGPRDCTTICYGGW-VDVWGP 138
DQ 60 YNDSLKGRITVSRDDSKNTFYQLQNSARAEDTAVYVCARGSH-----YFGHWHFAVMGQ 113
YDLSKGRITVSRDDSKNTFYQLQNSARAEDTAVYVCARGSH-----YFGHWHFAVMGQ 113
QY 139 GDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 198
DQ 114 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 173
GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 173
QY 199 FPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPC 258
DQ 174 FPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPC 233
FPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPC 233
QY 259 PAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
DQ 234 PAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
PAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
QY 319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
DQ 294 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 353
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 353
QY 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSK 438
DQ 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSK 413
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSK 413
QY 439 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
DQ 414 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 10
US-09-920-171-18
; Sequence 18, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Prestea, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-18

Query Match      81.2%; Score 2092; DB 10; Length 451;
Best Local Similarity 86.2%; Pred. No. 1.4e-107;
Matches 395; Conservative 19; Mismatches 36; Indels 8; Gaps 3;

QY 20 QVKLQWGEGLLOPSETLRTCTCVVSGSISGYVYVWIRQTQGRGLEWIGHYVGNATTN 79
DQ 1 EVQLVESGGGLVPGGSLRLSCAASGYSITSGYSMWIRQAPGKGLEWMSITYDG-STN 59
EVLVESGGGLVPGGSLRLSCAASGYSITSGYSMWIRQAPGKGLEWMSITYDG-STN 59
QY 80 YNPSLKSRVTISKDTSKNOFFLNLSVTDADTAVYVCARGPRDCTTICYGGW-VDVWGP 138
DQ 60 YNDSLKGRITVSRDDSKNTFYQLQNSARAEDTAVYVCARGSH-----YFGHWHFAVMGQ 113
YDLSKGRITVSRDDSKNTFYQLQNSARAEDTAVYVCARGSH-----YFGHWHFAVMGQ 113
QY 139 GDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 198
DQ 114 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 173
GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 173
QY 199 FPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPC 258
DQ 174 FPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPC 233
FPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPC 233
QY 259 PAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
DQ 234 PAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
PAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
QY 319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
DQ 294 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 353
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 353
QY 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSK 438
DQ 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSK 413
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSK 413
QY 439 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
DQ 414 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
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QY 20 QVKLQWGEGLLOPSETLRTCTCVVSGSISGYVYVWIRQTQGRGLEWIGHYVGNATTN 79
DQ 1 EVQLVESGGGLVPGGSLRLSCAASGYSITSGYSMWIRQAPGKGLEWVASIKYSG-ETK 59
EVLVESGGGLVPGGSLRLSCAASGYSITSGYSMWIRQAPGKGLEWVASIKYSG-ETK 59
QY 80 YNPSLKSRVTISKDTSKNOFFLNLSVTDADTAVYVCARGPRDCTTICYGGW-VDVWGP 138
DQ 60 YNPSVKGRITISRDDSKNTFYQLQNSLRAEDTAVYVCARGSH-----YFGHWHFAVMGQ 113
YNPSVKGRITISRDDSKNTFYQLQNSLRAEDTAVYVCARGSH-----YFGHWHFAVMGQ 113
QY 139 GDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 198
DQ 114 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 173
GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 173
QY 199 FPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPC 258
DQ 174 FPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPC 233
FPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPC 233
QY 259 PAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
DQ 234 PAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
PAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
QY 319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
DQ 294 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 353
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 353
QY 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSK 438
DQ 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSK 413
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSK 413
QY 439 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
DQ 414 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 11
US-09-740-002-25
; Sequence 25, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-740-002-25

Query Match      80.5%; Score 2075.5; DB 10; Length 475;
Best Local Similarity 84.9%; Pred. No. 1.2e-106;
Matches 399; Conservative 25; Mismatches 43; Indels 3; Gaps 3;

QY 8 LLLVAAPRWLSQVKLOOWGEGLLQPSSETLSRTCTCVVSGSISGYVYVWIRQTQGRGLE 66
DQ 8 LFLVAVATRVLSQVQKQESGVVVKVKTETLTCTVSGFSLSNRPMGVTVIROPFGKALE 67
LFLVAVATRVLSQVQKQESGVVVKVKTETLTCTVSGFSLSNRPMGVTVIROPFGKALE 67
QY 67 WIGHYVGNATTNYPNLSKSRVTISKDTSKNOFFLNLSVTDADTAVYVCARGPRDCTT 126
WIGHYVGNATTNYPNLSKSRVTISKDTSKNOFFLNLSVTDADTAVYVCARGPRDCTT 126
DQ 68 WLGNIFSSD-EKSFSPSLKSRLLTTSQDTSRSQVLSLTNVDPVDTATYICARVGLDYNA 126
WLGNIFSSD-EKSFSPSLKSRLLTTSQDTSRSQVLSLTNVDPVDTATYICARVGLDYNA 126
QY 127 ICYGGWVDVWGPGLDVTVVSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 186
ICYGGWVDVWGPGLDVTVVSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 186
DQ 127 Y-ELYLDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 185
Y-ELYLDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 185
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; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-14

Query Match      81.5%; Score 2100; DB 10; Length 451;
Best Local Similarity 86.5%; Pred. No. 5.3e-108;
Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

QY 20 QVKLQWEGGLQPSVTLRTCTVWSGSGISGYIYTWIQTPOGRGLEWIGHIYNGATTN 79
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAFPGKLEWVASITYDG-STN 59
QY 80 YNPSLKSRVTISKDTSKNOFFLNLSVTDADTAVYVCARGPRDCTTICYGGW-VDVWGP 138
Db 60 YNPVSKGRITISRDDSKNTFYLMNSLRAEDTAVYVCARGSH-----YFGHWHFAVWGQ 113
QY 139 GDLVTYSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHT 198
Db 114 GTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHT 173
QY 199 FPAVLQSSGLYSLSSVTVVPSSSLGTQTVICNVNHPKSNTKVDKABPKSCDKHTHTCPPC 258
Db 174 FPAVLQSSGLYSLSSVTVVPSSSLGTQTVICNVNHPKSNTKVDKABPKSCDKHTHTCPPC 233
QY 259 PAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
Db 234 PAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
QY 319 KPREEQYNSTYRVSVSLTVLHQDLWLGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 378
Db 294 KPREEQYNSTYRVSVSLTVLHQDLWLGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 353
QY 379 TLPSPRDELTKQVSLTCLVKGYFSPYSDIAVESNGQPENNYKTTTPVLDSDGSFFLYSK 438
Db 354 TLPSPREEMTKNQVSLTCLVKGYFSPYSDIAVESNGQPENNYKTTTPVLDSDGSFFLYSK 413
QY 439 LTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 476
Db 414 LTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 8
US-09-920-171-16
; Sequence 16, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
```

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; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-16

Query Match      81.5%; Score 2100; DB 10; Length 451;
Best Local Similarity 86.5%; Pred. No. 5.3e-108;
Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

QY 20 QVKLQWEGGLQPSVTLRTCTVWSGSGISGYIYTWIQTPOGRGLEWIGHIYNGATTN 79
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAFPGKLEWVASITYDG-STN 59
QY 80 YNPSLKSRVTISKDTSKNOFFLNLSVTDADTAVYVCARGPRDCTTICYGGW-VDVWGP 138
Db 60 YNPVSKGRITISRDDSKNTFYLMNSLRAEDTAVYVCARGSH-----YFGHWHFAVWGQ 113
QY 139 GDLVTYSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHT 198
Db 114 GTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHT 173
QY 199 FPAVLQSSGLYSLSSVTVVPSSSLGTQTVICNVNHPKSNTKVDKABPKSCDKHTHTCPPC 258
Db 174 FPAVLQSSGLYSLSSVTVVPSSSLGTQTVICNVNHPKSNTKVDKABPKSCDKHTHTCPPC 233
QY 259 PAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
Db 234 PAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
QY 319 KPREEQYNSTYRVSVSLTVLHQDLWLGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 378
Db 294 KPREEQYNSTYRVSVSLTVLHQDLWLGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 353
QY 379 TLPSPRDELTKQVSLTCLVKGYFSPYSDIAVESNGQPENNYKTTTPVLDSDGSFFLYSK 438
Db 354 TLPSPREEMTKNQVSLTCLVKGYFSPYSDIAVESNGQPENNYKTTTPVLDSDGSFFLYSK 413
QY 439 LTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 476
Db 414 LTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 9
US-09-925-179-68
; Sequence 68, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 68
; LENGTH: 451
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RESULT 5

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US-09-925-179-66
; Sequence 66, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-1GE Antibodies (
; FILE REFERENCE: P0718P2C1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: FCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 66
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy cha
US-09-925-179-66

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: Sequence 65, Application US/09925179
: Publication No. US20030044858A1
: GENERAL INFORMATION:
: APPLICANT: Presta, Paula M.
: APPLICANT: Jardiou, Leonard G.
: TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
: FILE REFERENCE: P0718P2C1D1C1US
: CURRENT APPLICATION NUMBER: US/09/925,179
: CURRENT FILING DATE: 2001-08-08
: PRIOR APPLICATION NUMBER: US 08/466,163
: PRIOR FILING DATE: 1995-06-06
: PRIOR APPLICATION NUMBER: US 08/405,617
: PRIOR FILING DATE: 1995-03-15
: PRIOR APPLICATION NUMBER: US 08/185,899
: PRIOR FILING DATE: 1994-01-26
: PRIOR APPLICATION NUMBER: PCT/US92/06860
: PRIOR FILING DATE: 1992-08-14
: PRIOR APPLICATION NUMBER: US 07/879,495
: PRIOR FILING DATE: 1992-05-07
: PRIOR APPLICATION NUMBER: US 07/744,768
: PRIOR FILING DATE: 1991-08-14
: NUMBER OF SEQ ID NOS: 68
: SEQ ID NO 65
: LENGTH: 451
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8b of Table
US-09-925-179-65

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124.905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948.429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-124-905-12

Query Match      89.6%; Score 2309; DB 9; Length 476;
Best Local Similarity 91.2%; Pred. No. 2.1e-119;
Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

Qy 1 MKHLWFLLLVAAPRWLSQVKLQWGGELLPSETLSRTCVVSGGSIISGYVYWTWIRQT 60
Db 1 MKHLWFLLLVAAPRWLSQVKLQWGGELLPSETLSRTCVVSGGSIISGYVYWTWIRQT 60
Qy 61 PGKLEWIGHIYGCATTNYPNLSKSRVTISKDTSKNQFFLNLSVTDADTAVVYCARGP 120
Db 61 PGKLEWIGHIYGCATTNYPNLSKSRVTISKDTSKNQFFLNLSVTDADTAVVYCARGP 120
Qy 121 RPDCTTICGGVDVWVGPGDLVTUSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
Db 121 RPDCTTICGGVDVWVGPGDLVTUSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
Qy 181 EPTVSNWNGALTSQVHFPFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKV 240
Db 181 EPTVSNWNGALTSQVHFPFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKV 240
Qy 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300
Db 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300
Qy 301 EVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
Db 301 EVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
Qy 361 IEKTSKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVEHESNGQPENNY 420
Db 361 IEKTSKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVEHESNGQPENNY 420
Qy 421 KTTTPVLDSDGSGFFLYSKLTVDKSRWQOGNPFVSCVMHEALHNHYTOKLSLSPGK 476
Db 421 KTTTPVLDSDGSGFFLYSKLTVDKSRWQOGNPFVSCVMHEALHNHYTOKLSLSPGK 476

RESULT 4
US-09-948-429B-12
; Sequence 12, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; AND USE THEREOF AS
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
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;
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948.429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-948-429B-12

Query Match      89.6%; Score 2309; DB 9; Length 476;
Best Local Similarity 91.2%; Pred. No. 2.1e-119;
Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

Qy 1 MKHLWFLLLVAAPRWLSQVKLQWGGELLPSETLSRTCVVSGGSIISGYVYWTWIRQT 60
Db 1 MKHLWFLLLVAAPRWLSQVKLQWGGELLPSETLSRTCVVSGGSIISGYVYWTWIRQT 60
Qy 61 PGKLEWIGHIYGCATTNYPNLSKSRVTISKDTSKNQFFLNLSVTDADTAVVYCARGP 120
Db 61 PGKLEWIGHIYGCATTNYPNLSKSRVTISKDTSKNQFFLNLSVTDADTAVVYCARGP 120
Qy 121 RPDCTTICGGVDVWVGPGDLVTUSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
Db 121 RPDCTTICGGVDVWVGPGDLVTUSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
Qy 181 EPTVSNWNGALTSQVHFPFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKV 240
Db 181 EPTVSNWNGALTSQVHFPFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKV 240
Qy 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300
Db 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300
Qy 301 EVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
Db 301 EVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
Qy 361 IEKTSKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVEHESNGQPENNY 420
Db 361 IEKTSKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVEHESNGQPENNY 420
Qy 421 KTTTPVLDSDGSGFFLYSKLTVDKSRWQOGNPFVSCVMHEALHNHYTOKLSLSPGK 476
Db 421 KTTTPVLDSDGSGFFLYSKLTVDKSRWQOGNPFVSCVMHEALHNHYTOKLSLSPGK 476
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-905-4

Query Match      100.0%; Score 2577; DB 9; Length 476;
Best Local Similarity 100.0%; Pred. No. 4.6e-134;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKHLWFFLLVAAPRWLSSQVKLQWEGGLQPSSETLSRSCVVGSGSISGYYYWTWIRQT 60
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DB 61 PGRGLEWIGHIYGNAGATTNPSLKSRTISKDTSKNOFNLNSVTDADTAVVYCARGP 120
QY 121 RPDCTTICYGWVDVWVGPGDLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
DB 121 RPDCTTICYGWVDVWVGPGDLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
QY 181 EPTVTSWNSGALTSGVHTFPFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKV 240
DB 181 EPTVTSWNSGALTSGVHTFPFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKV 240
QY 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDP 300
DB 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDP 300
QY 301 EVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAP 360
DB 301 EVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAP 360
QY 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420
DB 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420
QY 421 KTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 476
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RESULT 2
US-09-948-429B-4
; Sequence 4, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
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; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-948-429B-4

Query Match      100.0%; Score 2577; DB 9; Length 476;
Best Local Similarity 100.0%; Pred. No. 4.6e-134;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKHLWFFLLVAAPRWLSSQVKLQWEGGLQPSSETLSRSCVVGSGSISGYYYWTWIRQT 60
DB 1 MKHLWFFLLVAAPRWLSSQVKLQWEGGLQPSSETLSRSCVVGSGSISGYYYWTWIRQT 60
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DB 61 PGRGLEWIGHIYGNAGATTNPSLKSRTISKDTSKNOFNLNSVTDADTAVVYCARGP 120
QY 121 RPDCTTICYGWVDVWVGPGDLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
DB 121 RPDCTTICYGWVDVWVGPGDLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
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DB 181 EPTVTSWNSGALTSGVHTFPFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKV 240
QY 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDP 300
DB 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDP 300
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DB 301 EVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAP 360
QY 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420
DB 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420
QY 421 KTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 476
DB 421 KTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 476

RESULT 3
US-10-124-905-12
; Sequence 12, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:14:52 ; Search time 18.2478 Seconds

(without alignments)
1531.829 Million cell updates/sec

Title: US-09-758-173-4

Perfect score: 2577

Sequence: 1 MKRLWFFLLVAAPRWLSQ.....MHEALHNYTKSLSPGK 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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2: /cgn2_6/ptodata/1/pubpaa/PTCT NEW PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06 PUBCOMB pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US10 PUBCOMB pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60 NEW PUB pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60 PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2577	100.0	476	9 US-10-124-905-4	Sequence 4, Appl
2	2577	100.0	476	9 US-09-948-429B-4	Sequence 4, Appl
3	2309	89.6	476	9 US-10-124-905-12	Sequence 12, Appl
4	2309	89.6	476	9 US-09-948-429B-12	Sequence 12, Appl
5	2103	81.6	451	9 US-09-925-179-66	Sequence 66, Appl
6	2100	81.5	451	9 US-09-925-179-65	Sequence 65, Appl
7	2100	81.5	451	10 US-09-920-171-14	Sequence 14, Appl
8	2100	81.5	451	9 US-09-920-171-16	Sequence 16, Appl
9	2099	81.5	451	9 US-09-925-179-68	Sequence 68, Appl
10	2092	81.2	431	10 US-09-920-171-18	Sequence 18, Appl
11	2075.5	80.5	475	10 US-09-740-002-25	Sequence 25, Appl
12	2073	80.4	478	9 US-10-124-905-8	Sequence 8, Appl
13	2073	80.4	478	9 US-09-948-429B-8	Sequence 8, Appl
14	2069	80.3	453	9 US-09-925-179-8	Sequence 8, Appl
15	2069	80.3	453	10 US-09-802-077-8	Sequence 8, Appl
16	2069	80.3	453	10 US-09-802-096-8	Sequence 8, Appl
17	2061.5	80.0	452	9 US-09-726-258-71	Sequence 71, Appl
18	2047.5	79.5	475	10 US-09-740-002-27	Sequence 27, Appl
19	2047	79.4	451	9 US-09-996-288-230	Sequence 230, Appl

20 2045.5 79.4 450 9 US-09-996-288-216 Sequence 216, App
21 2045.5 79.4 450 9 US-09-996-288-218 Sequence 218, App
22 2045.5 79.4 450 9 US-09-996-288-250 Sequence 250, App
23 2045.5 79.4 450 10 US-09-796-848A-43 Sequence 43, Appl
24 2045.5 79.4 450 10 US-09-796-848A-49 Sequence 49, Appl
25 2044.5 79.3 450 9 US-09-996-288-220 Sequence 220, App
26 2044.5 79.3 450 9 US-09-996-288-222 Sequence 222, App
27 2044.5 79.3 450 9 US-09-996-288-224 Sequence 224, App
28 2044.5 79.3 450 10 US-09-796-848A-37 Sequence 37, Appl
29 2044.5 79.3 450 10 US-09-796-848A-39 Sequence 39, Appl
30 2044.5 79.3 450 10 US-09-796-848A-41 Sequence 41, Appl
31 2044.5 79.3 731 10 US-09-825-012-46 Sequence 46, Appl
32 2044.5 79.3 741 10 US-09-825-012-55 Sequence 55, Appl
33 2044.5 79.3 451 10 US-09-822-698A-26 Sequence 26, Appl
34 2042.5 79.3 450 9 US-09-996-288-232 Sequence 232, App
35 2042.5 79.3 450 9 US-09-996-288-234 Sequence 234, App
36 2042.5 79.3 450 9 US-09-996-288-236 Sequence 236, App
37 2041.5 79.2 450 9 US-09-996-288-238 Sequence 238, App
38 2041.5 79.2 450 9 US-09-996-288-242 Sequence 242, App
39 2041.5 79.2 450 9 US-09-996-288-244 Sequence 244, App
40 2041.5 79.2 450 9 US-09-996-288-246 Sequence 246, App
41 2039.5 79.1 450 9 US-09-996-288-208 Sequence 208, App
42 2039.5 79.1 729 10 US-09-825-012-52 Sequence 52, Appl
43 2039.5 79.1 739 10 US-09-825-012-61 Sequence 61, Appl
44 2038.5 79.1 450 9 US-09-996-288-210 Sequence 210, App
45 2038.5 79.1 450 9 US-09-996-288-228 Sequence 228, App

ALIGNMENTS

RESULT 1

US-10-124-905-4

; Sequence 4, Application US/10124905

; Patent No. US20020166136A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/124,905

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/383,916

; FILING DATE:

; APPLICATION NUMBER: US 08/487,550

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 476 amino acids

Db 414 LTVDKSRWQQGNVFCSCVMHEALHNHYTKLSLSPGK 451

RESULT 15

US-09-296-005-16

; Sequence 16, Application US/09296005

; Patent No. 6290957

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides

; FILE REFERENCE: P1123C1r

; CURRENT APPLICATION NUMBER: US/09/296,005

; CURRENT FILING DATE: 1999-04-21

; EARLIER APPLICATION NUMBER: US 08/887,352

; EARLIER FILING DATE: 1997-07-02

; NUMBER OF SEQ ID NOS: 26

; SEQ ID NO 16

; LENGTH: 451

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; NAME/KEY: Artificial

; LOCATION: 1-451

; OTHER INFORMATION: Heavy chain sequence derived from MAb11

US-09-296-005-16

Query Match 81.5%; Score 2100; DB 4; Length 451;

Best Local Similarity 86.5%; Pred. No. 1.5e-166;

Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

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Db 1 EVQLVESGGGLVQPGGSLRLSCAAGSYISITSGYSWNIQAPKGLEWVASITYDG-STN 59

QY 80 YNPILKSRVTISKDTSKNOFFNLNLSVTDADTAVYICARGPRDCTTICYGW-VDVNMP 138

Db 60 YNPVKGRTISRDDSKNTFYLQMNRAEDTAVYICARGSH-----YFGHWHFAVMGQ 113

QY 139 GDLAVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT 198

Db 114 GTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT 173

QY 199 FPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKKAEPKSCDKTHTCPPC 258

Db 174 FPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKKAEPKSCDKTHTCPPC 233

QY 259 PAPELLGGPSVFLFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318

Db 234 PAPELLGGPSVFLFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293

QY 319 KPREEQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVY 378

Db 294 KPREEQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVY 353

QY 379 TLPSPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK 438

Db 354 TLPSPREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK 413

QY 439 LTVDKSRWQQGNVFCSCVMHEALHNHYTKLSLSPGK 476

Db 414 LTVDKSRWQQGNVFCSCVMHEALHNHYTKLSLSPGK 451

Search completed: March 29, 2003, 09:17:41

Job time : 18.9126 secs

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QY 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
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QY 439 LTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 476
Db 414 LTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 451

RESULT 13
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-16

Query Match 81.5%; Score 2100; DB 4; Length 451;
Best Local Similarity 86.5%; Pred. No. 1.5e-166;
Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;
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Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASITVDG-STN 59
QY 80 YNPSLKSRTVTSKDTSKNOFFLNLSVTDADTAVYVCARGPRPDCTTICVGGW-VDVWGP 138
Db 60 YNPSVKGRITISRDDSKNTFYLMNSLRADTAVYVCARGSH-----YFGHHFAVWQ 113
QY 139 GDLVTSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVTVMNSGALTSQVHT 198
Db 114 GTLVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVTVMNSGALTSQVHT 173
QY 199 FPAVLQSSGLYLSVVTVTPSSSLGTQTYICNVNHPKNTKVDKAPKSCDKTHTCPPC 258
Db 174 FPAVLQSSGLYLSVVTVTPSSSLGTQTYICNVNHPKNTKVDKAPKSCDKTHTCPPC 233
QY 259 PAPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
Db 234 PAPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
QY 319 KPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKISKAKGQPREPQVY 378
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QY 319 KPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKISKAKGQPREPQVY 378
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RESULT 14
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; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/987,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-14

Query Match 81.5%; Score 2100; DB 4; Length 451;
Best Local Similarity 86.5%; Pred. No. 1.5e-166;
Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;
QY 20 QVKLQWGGELLPSETLSRTCVVSGSISGYIYWTWIRQTPGRGLEWIGHIYNGATTN 79
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASITVDG-STN 59
QY 80 YNPSLKSRTVTSKDTSKNOFFLNLSVTDADTAVYVCARGPRPDCTTICVGGW-VDVWGP 138
Db 60 YNPSVKGRITISRDDSKNTFYLMNSLRADTAVYVCARGSH-----YFGHHFAVWQ 113
QY 139 GDLVTSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVTVMNSGALTSQVHT 198
Db 114 GTLVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVTVMNSGALTSQVHT 173
QY 199 FPAVLQSSGLYLSVVTVTPSSSLGTQTYICNVNHPKNTKVDKAPKSCDKTHTCPPC 258
Db 174 FPAVLQSSGLYLSVVTVTPSSSLGTQTYICNVNHPKNTKVDKAPKSCDKTHTCPPC 233
QY 259 PAPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
Db 234 PAPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
QY 319 KPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKISKAKGQPREPQVY 378
Db 294 KPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKISKAKGQPREPQVY 353
QY 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
Db 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 413
QY 439 LTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 476

QY 139 GDLVTSSASTKGPSVRLPAPSSKSTSGTAAAGCLVKDYFPPVTVSNWNSGALTSGVHT 198
DB 114 GTLVTVSSASTKGPSVRLPAPSSKSTSGTAAAGCLVKDYFPPVTVSNWNSGALTSGVHT 173
QY 199 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGPREPQVY 258
DB 174 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGPREPQVY 233
QY 259 PAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
DB 234 PAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
QY 319 KPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGPREPQVY 378
DB 294 KPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGPREPQVY 353
QY 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSK 438
DB 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSK 413
QY 439 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
DB 414 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 11

US-08-466-151-65
; Sequence 65, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-65

Query Match 81.5%; Score 2100; DB 3; Length 451;
Best Local Similarity 86.5%; Pred. No. 1.5e-166;
Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

QY 20 QVKLQOMGGELLPQSETLSRSTCVSGGSGISGYVYWTMIROTPGRGLEWIGHYVNGATTN 79
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIROAPAGKLEWASITVDG-STN 59
QY 80 YNPILSKRVITISKDTSKNQFFLNLSVTDADTAVYYCARGPRPDCTTCYGGW-VDVWGP 138
DB 60 YNPISVGRITISRDTSKNTFYLMNSLRAEDTAVYYCARGSH-----YFCHWHFAVMGQ 113
QY 139 GDLVTSSASTKGPSVFLPAPSSKSTSGTAAAGCLVKDYFPPVTVSNWNSGALTSGVHT 198
DB 114 GTLVTVSSASTKGPSVFLPAPSSKSTSGTAAAGCLVKDYFPPVTVSNWNSGALTSGVHT 173
QY 199 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGPREPQVY 258
DB 174 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGPREPQVY 233
QY 259 PAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
DB 234 PAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
QY 319 KPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGPREPQVY 378
DB 294 KPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGPREPQVY 353
QY 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSK 438
DB 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSK 413
QY 439 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
DB 414 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 12

US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14

Query Match 81.5%; Score 2100; DB 4; Length 451;
Best Local Similarity 86.5%; Pred. No. 1.5e-166;
Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

QY 20 QVKLQOMGGELLPQSETLSRSTCVSGGSGISGYVYWTMIROTPGRGLEWIGHYVNGATTN 79
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIROAPAGKLEWASITVDG-STN 59

Db 175 EPTVSMNSGALTSVHTPAPVQLSSGLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKVCDHKPSNTKV 234

Qy 241 DKAEKPSKDKTHTCPCAPPELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDP 300

Db 235 DKVESK--YGPCCSPAPFEGGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDP 291

Qy 301 EVKFNWYVVDGVEVHNNAKTPREEQNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAP 360

Db 292 EVQFNWYVVDGVEVHNNAKTPREEQNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAP 351

Qy 361 IEXTISKAKQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420

Db 352 IEXTISKAKQPREPOVYTLPSQSEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 411

Qy 421 KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 476

Db 412 KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 467

RESULT 9

US-08-887-352B-14

; Sequence 14, Application US/08887352B

; Patent No. 5994511

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of

; TITLE OF INVENTION: Improving Polypeptides

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/887.352B

; FILING DATE: 03-Jul-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P1123

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 451 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-887-352B-14

Query Match 81.5%; Score 2100; DB 2; Length 451;

Best Local Similarity 86.5%; Pred. No. 1.5e-166;

Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

Qy 20 QVKLQWQEGGLQPSSTLSRTCVSGSGISGYVYWTWIRQTPGRLGLEWIGHYNGATTN 79

Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASIYDG-STN 59

Qy 80 YNPFLSKRVITISKDTSKNQVFLNLSVTDADTAVYVCARGPRPDCTTCYGGW-VDVWGP 138

Db 60 YNPFSVKGRTISRDDSKNTFYQLMNSLRADTAVYVCARGSH-----YFCHWHFAVWQ 113

Qy 139 GDLVTYSSASTKGPSVFFLAPSSKSTSGTAAALGCLVKDYPPEPVTVMNSGALTSVHT 198

Db 114 GTLVTVSSASTKGPSVFFLAPSSKSTSGTAAALGCLVKDYPPEPVTVMNSGALTSVHT 173

Qy 199 FPAVLQSSGLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKVCDHKPSKDKTHTCPC 258

Db 174 FPAVLQSSGLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKVCDHKPSKDKTHTCPC 233

Qy 259 PABELLGGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVVDGVEVHNNAK 318

Db 234 PABELLGGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVVDGVEVHNNAK 293

Qy 319 KPREEQNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKQPREPOVY 378

Db 294 KPREEQNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKQPREPOVY 353

Qy 379 TLPSPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK 438

Db 354 TLPSPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK 413

Qy 439 LTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 476

Db 414 LTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 451

RESULT 10

US-08-887-352B-16

; Sequence 16, Application US/08887352B

; Patent No. 5994511

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of

; TITLE OF INVENTION: Improving Polypeptides

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/887.352B

; FILING DATE: 03-Jul-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P1123

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 451 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-887-352B-16

Query Match 81.5%; Score 2100; DB 2; Length 451;

Best Local Similarity 86.5%; Pred. No. 1.5e-166;

Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

Qy 20 QVKLQWQEGGLQPSSTLSRTCVSGSGISGYVYWTWIRQTPGRLGLEWIGHYNGATTN 79

Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASIYDG-STN 59

Qy 80 YNPFLSKRVITISKDTSKNQVFLNLSVTDADTAVYVCARGPRPDCTTCYGGW-VDVWGP 138

Db 60 YNPFSVKGRTISRDDSKNTFYQLMNSLRADTAVYVCARGSH-----YFCHWHFAVWQ 113

RESULT 7

```

US-08-397-411-7
: Sequence 7, Application US/08397411
: Patent No. 6129914
: GENERAL INFORMATION:
: APPLICANT: Weiner, George
: APPLICANT: Gingrich, Roger
: APPLICANT: Link, Brian
: APPLICANT: Teo, J. Yun
: TITLE OF INVENTION: Bispecific Antibody Effective to Treat
: TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew
: STREET: One Market plaza, Steuart Tower, Suite 2000
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94105
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent'n Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/397,411
: FILING DATE: 01-MAR-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/859,583
: FILING DATE: 27-MAR-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M.
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 011823-004901
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-326-2400
: TELEFAX: 415-326-2422
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 446 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-397-411-7

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320	PREEQNSTYRWISVLTLHQDWLNGEYCKVKSNKALPAPIETIKSAKGQPREPOVYT	379
Qy		
290	PREEQNSTYRWISVLTLHQDWLNGEYCKVKSNKALPAPIETIKSAKGQPREPOVYT	349
Db		
380	LPSPRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSGFFLYSKL	439
Qy		
350	LPSPRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSGFFLYSKL	409
Db		
440	TVDKSRQOQGVNFCSVMHREALNHHYTKQSLSLSPGK	476
Qy		
410	TVDKSRQOQGVNFCSVMHREALNHHYTKQSLSLSPGK	446
Db		

RESULT 8

```

US-08-523-894-10
; Sequence 10, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-523-894-10

```

Query Match	81.7%;	Score 2106.5;	DB 3;	Length 446;
Best Local Similarity	88.2%;	Pred. No. 4.1e-167;		
Matches 403; Conservative	16;	Mismatches 27;	Indels 11;	Gaps 4;

NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELEPHONE: 703-836-6620
TELEFAX: 703-836-6620
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-523-894-12

Query Match 82.0%; Score 2112.5; DB 4; Length 467;
Best Local Similarity 84.5%; Pred. No. 1.4e-167;
Matches 402; Conservative 24; Mismatches 41; Indels 9; Gaps 2;

QY 1 MKHLWFFLLVAAPRWLSQVKLQWEGGLQPSVTLRTCTCVVSGGSGYGYWTWIROT 60
DB 1 MKHLWFFLLVAAPRWLSQVKLQWEGGLQPSVTLRTCTCVVSGGSGYGYWTWIROT 60
QY 61 PGRGLEWIGHIYNGGATTNNPSLKRVTISKDTSKNQFFLNLSVTDADTAVVYCA 120
DB 61 PGRGLEWIGHIYNGGATTNNPSLKRVTISKDTSKNQFFLNLSVTDADTAVVYCA 117
QY 121 RPDCTTCYGGWVDVWPGDLVTVSSASTKGPSPVPLAPSSKSTSGTAAALGCLVKDYFP 180
DB 118 ---SNILKYLHLLYWGQGLVTVSSASTKGPSPVPLAPSSKSTSGTAAALGCLVKDYFP 174
QY 181 EPTVTSWNSGALTSVGHVTPPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNTKV 240
DB 175 EPTVTSWNSGALTSVGHVTPPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNTKV 234
QY 241 DKAEKPSKDKTHCTPCPAPELLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDP 300
DB 235 DKRVESK---YGPCCPCPAPEFGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDP 291
QY 301 EVKFNWYVDGVEVHNKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
DB 292 EVQFNWYVDGVEVHNKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 351
QY 361 IEKTIKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
DB 352 IEKTIKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 411
QY 421 KTTTPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 476
DB 412 KTTTPVLDSDGSPFLYSRLTVDKSRWQEGNVFCSCVMHEALHNNHYTKQSLSLSLGK 467

RESULT 6

US-08-523-894-8

; Sequence 8, Application US/08523894

; Patent No. 6136310

GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELEPHONE: 703-836-6620
TELEFAX: 703-836-6620
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-523-894-8

Query Match 81.9%; Score 2111.5; DB 4; Length 467;
Best Local Similarity 84.5%; Pred. No. 1.7e-167;
Matches 402; Conservative 24; Mismatches 41; Indels 9; Gaps 2;

QY 1 MKHLWFFLLVAAPRWLSQVKLQWEGGLQPSVTLRTCTCVVSGGSGYGYWTWIROT 60
DB 1 MKHLWFFLLVAAPRWLSQVKLQWEGGLQPSVTLRTCTCVVSGGSGYGYWTWIROT 60
QY 61 PGRGLEWIGHIYNGGATTNNPSLKRVTISKDTSKNQFFLNLSVTDADTAVVYCA 120
DB 61 PGRGLEWIGHIYNGGATTNNPSLKRVTISKDTSKNQFFLNLSVTDADTAVVYCA 117
QY 121 RPDCTTCYGGWVDVWPGDLVTVSSASTKGPSPVPLAPSSKSTSGTAAALGCLVKDYFP 180
DB 118 ---SNILKYLHLLYWGQGLVTVSSASTKGPSPVPLAPSSKSTSGTAAALGCLVKDYFP 174
QY 181 EPTVTSWNSGALTSVGHVTPPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNTKV 240
DB 175 EPTVTSWNSGALTSVGHVTPPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNTKV 234
QY 241 DKAEKPSKDKTHCTPCPAPELLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDP 300
DB 235 DKRVESK---YGPCCPCPAPEFGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDP 291
QY 301 EVKFNWYVDGVEVHNKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
DB 292 EVQFNWYVDGVEVHNKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 351
QY 361 IEKTIKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
DB 352 IEKTIKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 411
QY 421 KTTTPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 476
DB 412 KTTTPVLDSDGSPFLYSRLTVDKSRWQEGNVFCSCVMHEALHNNHYTKQSLSLSLGK 467

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANTCUT01
CLONE: 1513264
US-09-049-672A-4

Query Match 88.4%; Score 2277.5; DB 4; Length 473;
Best Local Similarity 90.8%; Pred. No. 2.7e-181;
Matches 434; Conservative 16; Mismatches 21; Indels 7; Gaps 4;
QY 1 MKHLWFFLLVAAPRWLSQVKLQWGEGLLOPSETLSRTCVVSGSI-SGYYYWTWIRQ 59
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QY 60 TPGGLEWHIYGNGATTNPNLSKRVTSKDTSKNQFFLNLSVTDADTAVYICAR 119
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QY 120 PRDCTTCYGVG-VDMWPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 178
DB 119 ---DVLGRGGNMDVWGGLTTLVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 175
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DB 176 FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNT 235
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QY 299 DPEVKNWYDGVGEVHNATKPREEQYNSTYRVSVLTVLHQDLNKGKEYCKVSNKALP 358
DB 296 DPEVKNWYDGVGEVHNATKPREEQYNSTYRVSVLTVLHQDLNKGKEYCKVSNKALP 355
QY 359 APIEKTISKAKGPQPVVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 418
DB 356 APIEKTISKAKGPQPVVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 415
QY 419 NYKTPPVLDSDGSFFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 476
DB 416 NYKTPPVLDSDGSFFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 473

RESULT 4
US-08-793-450-8
Sequence 8, Application US/08793450
Patent No. 6312690
GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-793-450-8
Query Match 85.6%; Score 2206; DB 4; Length 472;
Best Local Similarity 90.0%; Pred. No. 2.4e-175;
Matches 422; Conservative 9; Mismatches 34; Indels 4; Gaps 3;
QY 8 LLLVAAPRWLSQVKLQWGEGLLOPSETLSRTCVVSGSISGYYYWTWIRQTPGRGLEW 67
DB 8 LFLVATATGVHSQVQLQWAGLLKPKSETLSLCTVYGSFSG-YWMSWIRQPPGKLEW 66
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DB 67 IGEINHSQ-STNPNLSKRVTSISVDTSKNQFSLKLSVTAADTAVYICARA--PEYKWK 123
QY 128 CYGWDVDMWPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 187
DB 124 YHGMDFDPMWGGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 183
QY 188 NSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKDKAEPK 247
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DB 364 AKGPQPVVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 423
QY 428 DSDGSFFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 476
DB 424 DSDGSFFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 472
RESULT 5
US-08-523-894-12
Sequence 12, Application US/08523894
Patent No. 6136310
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy

QY 61 PGRGLEWIGHIYNGGATTNNPSLKSRTVTSKDTSKNQFFLNLSVTDADTAVYICARGP 120
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RESULT 2

US-08-487-550-12
; Sequence 12, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-12

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Best Local Similarity 91.2%; Pred. No. 6.6e-184;

Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;
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RESULT 3
US-09-049-672A-4
; Sequence 4, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US

Db 661 GTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTT 718

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Best Local Similarity 91.4%; Pred. No. 1.3e-162;
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Job time : 2261.24 secs

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Qy 541 TCGGGTAACTCCAGAGAGTGTCAAGAGCAGGACAGCAAGGACACCTACAGCTC 600
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Qy 601 AGCAGACCTCAGCTGAGCTGAGCAAGAGCTTCAAAAGAGCTTCAACAGGGGAGAGTGT 718
Db 601 AGCAGACCTCAGCTGAGCTGAGCAAGAGCTTCAAAAGAGCTTCAACAGGGGAGAGTGT 718
Qy 661 GTCAACCATCAGGGCTGAGCTGCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 718
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RESULT 14
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LOCUS
DEFINITION
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720 bp DNA linear PAT 31-JAN-2002
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protein Human monoclonal antibody against parathyroid
hormone-related protein Human monoclonal antibody against
parathyroid hormone-related protein Human monoclonal antibody
against parathyroid hormone-related protein Human monoclonal
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monoclonal antibody against parathyroid hormone-related protein.
E35204
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hori,N., Kusunoki,C. and Kamata,M.
Human monoclonal antibody against parathyroid hormone-related
Patent: JP 2000080100-A 4 21-MAR-2000;
JAPAN TOBACCO INC
OS Homo sapiens (human)
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.PF , 12-OCT-1998 JP 1998304793

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Best Local Similarity 89.4%; Pred. No. 1.1e-162;
Matches 642; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
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KEYWORDS     JP 2000080100-A/7.
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             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 720)
AUTHORS      Hori,N., Kusunoki,C. and Kamata,M.
TITLE        Human monoclonal antibody against parathyroid hormone-related
JOURNAL      Patent: JP 2000080100-A 7 21-MAR-2000;
COMMENT      JAPAN TOBACCO INC
OS           Homo sapiens (human)
PN           JP 2000080100-A/7
PD           21-MAR-2000
PF           12-OCT-1998  JP 1998304793
PR
PI           NOBUAKI HORI, CHIIHIRO KUSUNOKI, MASASHI KAMATA
PC           C07K16/26, A61K31/00, A61K31/00, A61K31/00, A61K31/00, A61K31/00,
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DEFINITION Human monoclonal antibody against parathyroid hormone-related
            protein.
ACCESSION   E35208
VERSION     E35208.1  GI:18624436
KEYWORDS   JP 2000080100-A/8.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 720)
AUTHORS     Hori,N., Kusunoki,C. and Kamata,M.
TITLE       Human monoclonal antibody against parathyroid hormone-related
JOURNAL     Patent: JP 2000080100-A 8 21-MAR-2000;
COMMENT     JAPAN TOBACCO INC
OS           Homo sapiens (human)
PN           JP 2000080100-A/8
PD           21-MAR-2000
PF           12-OCT-1998  JP 1998304793
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PI           NOBUAKI HORI, CHIIHIRO KUSUNOKI, MASASHI KAMATA
PC           C07K16/26, A61K31/00, A61K31/00, A61K31/00, A61K31/00, A61K31/00,
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DEFINITION E35205 Human monoclonal antibody against parathyroid hormone-related protein.
ACCESSION E35205
VERSION E35205.1 GI:18624433
KEYWORDS JP 2000080100-A/5.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 720)
Hori,N., Kusunoki,C. and Kamata,M.
TITLE Human monoclonal antibody against parathyroid hormone-related protein.
JOURNAL Patent: JP 2000080100-A 5 21-MAR-2000; JAPAN TOBACCO INC
COMMENT OS Homo sapiens (human)
PN JP 2000080100-A/5
PD 21-MAR-2000
PF 12-OCT-1998 JP 1998304793
PR
PI NORUAKI HORI, CHIHIRO KUSUNOKI, MASASHI KAWATA
PC C07K16/26;A61K31/00;A61K31/00;A61K31/00;A61K31/00;A61K31/00,
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RESULT 12
E35207
LOCUS Human monoclonal antibody against parathyroid hormone-related protein.
DEFINITION E35207 Human monoclonal antibody against parathyroid hormone-related protein.
ACCESSION E35207
DNA 720 bp linear PAT 31-JAN-2002
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AX067347
LOCUS AX067347 963 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 51 from Patent WO0078960.
ACCESSION AX067347
VERSION AX067347.1 GI:12544971
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 963)
AUTHORS Yuqiu, J. and Mitcham, J.L.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: WO 0078960-A 51 28-DEC-2000;
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DEFINITION Homo sapiens IGK mRNA for immunoglobulin kappa light chain VLJ region, partial cds, clone:K65.
ACCESSION AB064106
VERSION AB064106.1 GI:21669418
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.
TITLE Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 830)
AUTHORS Kurosawa, Y.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyoake 470-1192, Japan
(E-mail: kurosawa@fujita-hu.ac.jp, tel:81-562-93-9387)
COMMENT Please visit our web site
URL: http://www.fujita-hu.ac.jp/immunity/.
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DEFINITION Homo sapiens, clone MGC:22745 IMAGE:4251290, mRNA, complete cds.
ACCESSION BC030814
VERSION BC030814.1 GI:21410816
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 972)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LILNL at: http://image.llnl.gov
Series: IRAL Plate: 35 Row: e Column: 23
This clone was selected for full length sequencing because it
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Qy 241 TCTGGGTGCCAGACAGATTTCAGCGCAGTGGGCGGAGGACAGATTTCACACTGMAAATC 300
Db 271 TCCGGGTGCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTACACTGMAAATC 330
Qy 301 AGCCAGTGGAGGCTGAAGATGTTGGGTTTATTTCTCGCGGCAAGGTACAAGACTCCT 360
Db 331 AGCAAGTGGAGGCTGAGGATGTTGGGATTTATTACTGCATGCAAGGTCTACAACTCCT 390
Qy 361 CCCACTTTCCGGCGGAGGACCAAGGTGGAATCAAACTGAGGTGGCTGCACCATCTGTC 420
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Db 451 TTCATCTCCCGCCATCTGATGAGCAGTTCGAAATCTGGAATCTGCTGTTGTGCTGCTG 510
Qy 481 CTGAATAACTTCTATCCAGAGAGCCAAAGTACAGTGAAGGTGGATAAGCCCTCCAA 540
Db 511 CTGAATAACTTCTATCCAGAGAGCCAAAGTACAGTGAAGGTGGATAAGCCCTCCAA 570
Qy 541 TCGGTAAGTCCCGCCATCTGATGAGCAGTTCAGAGCAGGACAGCAAGGACCTACAGCTC 600
Db 571 TCGGTAAGTCCCGCCATCTGATGAGCAGTTCAGAGCAGGACAGCAAGGACCTACAGCTC 630
Qy 601 AGCAGCCTCCGCTGAGCCTGAGCAAGAGCAGTTCAGAGAAACAAAGTCTACGCTCGGAA 660
Db 631 AGCAGCCTCCGCTGAGCCTGAGCAAGAGCAGTTCAGAGAAACAAAGTCTACGCTCGGAA 690
Qy 661 GTCAACCATCAGGCGCTGAGCTGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 718
Db 691 GTCAACCATCAGGCGCTGAGCTGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 748
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RESULT 6		270 bp	DNA	linear	PAT 31-JAN-2002
E40697	Antihuman Fas humanized antibody-containing antirheumatic.				
LOCUS	E40697				
DEFINITION	Antihuman Fas humanized antibody-containing antirheumatic.				
ACCESSION	E40697				
VERSION	E40697.1	GI:18627286			
KEYWORDS	JP 2000154149-A/68.				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 720)				
AUTHORS	Srizawa,N., Haryuama,H., Takahashi,W., Nakahara,K. and Yonehara,S.				
TITLE	Antihuman Fas humanized antibody-containing antirheumatic				
JOURNAL	Patent: JP 2000154149-A 68 06-JUN-2000;				
COMMENT	SANKYO CO LTD				
	OS Artificial Sequence				
	PN JP 2000154149-A/68				
	PD 06-JUN-2000				
	PF 17-SEP-1999 JP 1999263984				
	PR				
	PI NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,WATARU TAKAHASHI, PI KAORI NAKAHARA,				
	PI SHIN YONEHARA				
	PC A61K39/395,A61P29/00,C12N15/09//C07K16/28,C12P21/02,C12N15/00				
	CC				
	Key	Location/Qualifiers			
	FT CDS	(1)..(717)			
	FT mat_peptide	(61)..(717)			
	FT sig_peptide	(1)..(61)			
		Location/Qualifiers			
		1..720			
		/organisms="synthetic construct"			
		/db xref="taxon:32630"			
BASE COUNT	179 a 200 c 185 g 156 t				
ORIGIN					
	Query Match	85.9%	Score 618.8;	DB 6;	Length 720;
	Best Local Similarity	91.4%	Pred. No. 1.2e-168;		
	Matches 656;	Conservative 0;	Mismatches 62;	Indels 0;	Gaps 0;
QY	1	ATGAGCTCCCTGCTCAGCTCCTCGGCTGCTATGCTGCTGCTCCCGGTCCAGTGGG	60		
Db	1	ATGAGGCTCCCTGCTCAGCTCCTCGGCTGCTGTAATGCTCTGGTCCAGGATCCAGTGGG	60		
QY	61	GAAGTGTGATGACTCAGTCTCCACTGCTCCCTCCCATCACCTCGAGAGCGGCTCC	120		
Db	61	GATGTTGTGATGACTCAGTCTCCACTCTCCCTCGGCTCACCTTTGGACAGCGGCTCC	120		
QY	121	ATCTCTGTAGTCTAGTCAAAAGCTTTAAACACAGTAATGGAGACACCTTCTCAGTGG	180		
Db	121	ATCTCTGCAGATCTAGTAAGAGCCTTTGTACACAGTAATGGAAACACCTATTTACATGG	180		
QY	181	TATCAGCAGAGAGCCAGCCCAACTCCAAAGGCTCTGATTTATTAAGGTTCTTAACCGGAC	240		
Db	181	TACCTGCAGAAGCCAGCCCAAGTCTCCAAAGGCTCTGATCTACAAAGTTTCCAAACCGATT	240		
QY	241	TCTGGGGTCCAGACAGATTACAGCGGAGTGGGCGAGGACAGATTTCACACTGAAATC	300		
Db	241	TCTGGGGTCCAGACAGATTACAGCGGAGTGGGTCAGGCACTGATTTTCACACTGAAATC	300		
QY	301	AGCGAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTCGCGGGCAAGGTACAAGGACTCCT	360		
Db	301	AGCAGGCTGAGGCTGAGGATGTTGGGGTTTATTTACTGCTCTCAAAGTACACATGTTCT	360		
QY	361	CCACATTTCCGGCGGAGGACAGAGGTGGAAATCAACGTAACGTTGGGTGCAACCATGTGC	420		
Db	361	CCGGCGTTCGGCCAAAGGACCAAGGTGGAAATCAACGTAACGTTGGGTGCAACCATGTGC	420		
QY	421	TTCACTTTCCGGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCCTGTGTGTGCGCTG	480		
Db	421	TTCACTTTCCGGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCCTGTGTGTGCGCTG	480		
QY	481	CTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATTAACAGCGCTCCAA	540		

Db	481	CTGAATAAATCTTCTATCCAGAGAGCCAAAGTACAGTGGAAAGTGGATAACGCCCTCCAA	540
Qy	541	TCGGGTAACTCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGACCTACAGCCTC	600
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Qy	601	AGCAGCACCTCTGACGCTCAGCAAGCAGACTACGAGAAACAACAAAGTCTACGCCCTCGCAA	660
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Qy	661	GTACCCCATCAGGGCCTCAGCTCGCCCTCTCAAAAGACTTTCACAGGGGAGAGTGTT	718
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RESULT 7			
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LOCUS	E40695	720 bp	DNA
DEFINITION	Antihuman Fas humanized antibody-containing antirheumatic.		linear
ACCESSION	E40695		PAT 31-JAN-2002
VERSION	E40695.1	GI:18627284	
KEYWORDS	JP 2000154149-A/66.		
SOURCE	synthetic construct.		
ORGANISM	synthetic construct		
REFERENCE	artificial sequences.		
AUTHORS	1 (bases 1 to 720)		
TITLE	Serizawa,N., Haruyama,H., Takahashi,W., Nakahara,K. and Yonehara,S.		
JOURNAL	Antihuman Fas humanized antibody-containing antirheumatic		
COMMENT	Patent: JP 2000154149-A 66 06-JUN-2000;		
	SANKYO CO LTD		
	OS Artificial Sequence		
	PN JP 2000154149-A/66		
	PD 06-JUN-2000		
	PF 17-SEP-1999 JP 1999263984		
	PR		
	PI NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,WATARU TAKAHASHI, PI KAORI NAKAHARA.		
	PN SHIN YONEHARA		
	PC A61K39/395,A61P29/00,C12N15/09//C07K16/28,C12P21/02,C12N15/00		
	CC		
	Key	Location/Qualifiers	
	PH CDS	(1)..(717)	
	FT mat_peptide	(61)..(717)	
	FT sig_peptide	(1)..(60).	
FEATURES	Location/Qualifiers		
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BASE COUNT	180 a 200 c 184 g 156 t		
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Query Match	85.74;	Score 617.2;	DB 6; Length 720;
Best Local Similarity	91.24;	Pred. No. 3.4e-168;	
Matches	655; Conservative	0; Mismatches 63; Indels 0; Gaps 0;	
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Db	1	ATGAGGCTCCCTGCTCAGCTCCTCGGGCTGCTATGTCTGCGTCCCGGGTCCAGTGGG	60
Qy	61	GAAAGTTGTGATGACTCAGTCTCCACTGTCCTTCCCATCACCTCGAGAGCCGGCTCC	120
Db	61	GATGTTGTGATGACTCAGTCTCCACTGTCCTGCGCTCACCTTTGACAGCCGGCTCC	120
Qy	121	ATCTCTGTAGTCTAGTCAAAGCTTTAAACACAGTAATGGAGACACCTTCTCGATTGG	180
Db	121	ATCTCTGCAGATCTAGTAAGAGCCTTGTAACACAGTAATGGAACACACTATTTACATTGG	180
Qy	181	TATCAGCAGAAGCCAGCCCACTCCGAAGGCTCCTGATTTATTAAGTTTCTTAACCGGAC	240
Db	181	TACCTGAGAAGCCAGCCCACTCTCCAAGCTCCTGATCTACAAAGTTTCCAAACCGATT	240
Qy	241	TCTGGGCTCCAGACAGATTTCAGCGGAGTGGGSCAGGACAGATTTTCACACTCAAAATC	300

BASE COUNT		204 a		267 c		225 g		195 t	
ORIGIN									
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Best Local Similarity		91.5%;		Pred. No. 4e-169;					
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Qy	61	GAAGTTGTGATGACTCAGTCTCCACTCTGCTCTCCCTTCCCATCACACTTGGAGAGCGGCTCC	120						
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Qy	361	CCACTTTTCGGCGGAGGACCAAGTGGGAATCAAACTGCTACGCTGGCTGACCACTCTGTC	420						
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Qy	421	TTTCATCTTCGCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCTTGTGTGCTCTG	480						
Db	461	TTTCATCTTCGCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCTTGTGTGCTCTG	520						
Qy	481	CTGAATAACTTCTATCCACAGAGGGCCAAAGTACAGTGGAAAGTGGATAACGCCCTCCAA	540						
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Db	641	AGCAGCACCTCTGAGCTGAGCAAAAGCAGACTACAGAAACACAAAGTCTAGCGCTCGGAA	700						
Qy	661	GTACCCCATCAGGGCTGAGCTCCCGTTCACAAAGCTTCAACGGGAGAGTGT	718						
Db	701	GTACCCCATCAGGGCTGAGCTCCCGTTCACAAAGCTTCAACGGGAGAGTGT	758						
RESULT 5									
E40696									
LOCUS		E40696							
DEFINITION		Anti-human Fas humanized antibody-containing antitirneumatic.							
ACCESSION		E40696							
VERSION		E40696.1 GI:18627285							
KEYWORDS		JP 2000154149-A/67.							
SOURCE		synthetic construct.							
ORGANISM		synthetic construct.							
REFERENCE		1 (bases 1 to 720).							
AUTHORS		Serizawa,N., Haruyama,H., Takahashi,W., Nakahara,K. and Yonehara,S.							
TITLE		Anti-human Fas humanized antibody-containing antitirneumatic							
JOURNAL		Patent: JP 2000154149-A 67 06-JUN-2000;							
COMMENT		SANKYO CO LTD							
		OS Artificial Sequence							

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RESULT 3
E40698
LOCUS Antihuman Fas humanized antibody-containing antirheumatic.
DEFINITION
ACCESSION E40698
VERSION E40698.1 GI:18627287
KEYWORDS JP 2000154149-A/69.
SOURCE synthetic construct.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 720).
AUTHORS Serizawa,N., Haruyama,H., Takahashi,W., Nakahara,K. and Yonehara,S.
TITLE Antihuman Fas humanized antibody-containing antirheumatic
JOURNAL Patent: JP 2000154149-A 69 06-JUN-2000;
SANKYO CO LTD
COMMENT OS Artificial Sequence
PN JP 2000154149-A/69
PD 06-JUN-2000
PF 17-SEP-1999 JP 1999263984
PR PI NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,WATARU TAKAHASHI, PI KAORI
NAKAHARA,
PC A61K39/395,A61P29/00,C12N15/09//C07K16/28,C12P21/02,C12N15/00
CC
FH Key Location/Qualifiers
FT CDS (1)..(717)
FT mat_peptide (61)..(717)
FT sig_peptide (1)..(160).
FT Location/Qualifiers
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source 1..720
BASE COUNT 177 a 200 c 186 g 157 t
ORIGIN

Query Match 85.4%; Score 622; DB 5; Length 720;
Best Local Similarity 91.6%; Pred. No. 1.4e-169;
Matches 658; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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Db 1 ATGAGCCCTCCCTGCTCAGCTCCTCGGGCTGTATTGTCTGCGCTCCCGGGTCCAGTGGG 60
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QY 61 GAAATGTGATGATCAGTCTCCACTGCTCCCTCCCATCACCTCGAGAGCGGCTCC 120
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Db 61 GATGTGTGATGATCAGTCTCCACTGCTCCCTCCCGCTCCCTTGGACAGCGGCTCC 120
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RESULT 4
E40748
LOCUS Antihuman Fas humanized antibody-containing antirheumatic.
DEFINITION
ACCESSION E40748
VERSION E40748.1 GI:18627337
KEYWORDS JP 2000154149-A/119.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 891).
AUTHORS Serizawa,N., Haruyama,H., Takahashi,W., Nakahara,K. and Yonehara,S.
TITLE Antihuman Fas humanized antibody-containing antirheumatic
JOURNAL Patent: JP 2000154149-A 119 06-JUN-2000;
SANKYO CO LTD
COMMENT OS Homo sapiens (human)
PN JP 2000154149-A/119
PD 06-JUN-2000
PF 17-SEP-1999 JP 1999263984
PR PI NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,WATARU TAKAHASHI, PI KAORI
NAKAHARA,
PC A61K39/395,A61P29/00,C12N15/09//C07K16/28,C12P21/02,C12N15/00
CC
FH Key Location/Qualifiers
FT CDS (1)..(891)
FT mat_peptide (61)..(891)
FT sig_peptide (1)..(160).
FT Location/Qualifiers
FEATURES
source 1..891
BASE COUNT 177 a 200 c 186 g 157 t
ORIGIN

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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:13:05 ; Search time 2259.24 Seconds
(without alignments)
9274.790 Million cell updates/sec

Title: US-09-758-173-5
Perfect score: 720
Sequence: 1 ATGAGCCCTCCCTGCTCAGCT.....TCAACAGGGGAGAGGTGGA 720

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

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37: em.htg.vrt.*

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39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	720	100.0	720	6	AR108864	Sequence
2	628.4	87.3	973	9	BC022362	BC022362 Homo sapi
3	622	86.4	720	6	E40698	E40698 Antihuman F
4	620.4	86.2	891	6	E40748	E40748 Antihuman F
5	618.8	85.9	720	6	E40696	E40696 Antihuman F
6	618.8	85.9	720	6	E40697	E40697 Antihuman F
7	617.2	85.7	720	6	E40695	E40695 Antihuman F
8	607.6	84.4	972	9	BC030814	BC030814 Homo sapi
9	601.2	83.5	963	6	AX067347	AX067347 Sequence
10	599.6	83.3	830	9	AB064106	AB064106 Homo sapi
11	599.4	83.2	720	6	E35205	E35205 Human monoc
12	599.4	83.2	720	6	E35207	E35207 Human monoc
13	598.8	83.2	720	6	E35208	E35208 Human monoc
14	598.2	83.1	720	6	E35204	E35204 Human monoc
15	598	83.1	830	9	AB064102	AB064102 Homo sapi
16	596.6	82.9	720	6	E35201	E35201 Human monoc
17	595.4	82.7	720	6	E35206	E35206 Human monoc
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25	580.4	80.6	794	9	AB064137	AB064137 Homo sapi
26	578.8	80.4	775	9	AB064133	AB064133 Homo sapi
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35	561.2	77.9	726	6	E10698	E10698 cDNA encodi
36	561.2	77.9	785	9	AB064055	AB064055 Homo sapi
37	556.4	77.3	784	9	AB064058	AB064058 Homo sapi
38	556.4	77.3	829	9	AB064112	AB064112 Homo sapi
39	554.8	77.1	857	9	AB064092	AB064092 Homo sapi
40	554.8	77.1	858	9	AB064091	AB064091 Homo sapi
41	554.8	77.1	858	9	AB064093	AB064093 Homo sapi
42	554.4	77.0	839	9	AB064089	AB064089 Homo sapi
43	549.2	76.3	740	6	AX076853	AX076853 Sequence
44	549.2	76.3	740	6	AX076855	AX076855 Sequence
45	532	73.9	660	6	AX277240	AX277240 Sequence

ALIGNMENTS

RESULT 1
AR108864 LOCUS
DEFINITION Sequence 5 from patent US 6113898.
ACCESSION AR108864
VERSION AR108864.1 GI:12825140
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 720)
AUTHORS Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
TITLE Human B7.1-specific primatized antibodies and transfectomas
expressing said antibodies
JOURNAL Patent: US 6113898-A 5 05-SEP-2000;

720 bp DNA linear PAT 14-FEB-2001

Db 241 TCCGGGGTCCCTGACAGGTTTCAGTGGCACTGGATCAGGCACAGATTTTACACTGAAAATC 300
Qy 301 AGCCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGCGGGCAAGGTACAAAGGACTCCT 360
Db 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTTCTGCGGGCAAGGTACAAAGGACTCCT 360
Qy 361 CCCACTTTCGGGGGAGGAGCCAAAGGTGGAAATCAAAAGTACGGTGGCTGGCAACCATCTGTC 420
Db 361 TTCACCTTTCGGGGCTGGGACCCAAAGTGGATATCAAAAGTACGGTGGCTGGCAACCATCTGTC 420
Qy 421 TTCAATCTTCCCGGCATCTGATGAGCAGTTGAAATCTGGAACTGCGCTCTCTGTTGTGCGCTG 480
Db 421 TTCAATCTTCCCGGCATCTGATGAGCAGTTGAAATCTGGAACTGCGCTCTCTGTTGTGCGCTG 480
Qy 481 CTGAATAACTTTCTATCCCGAGAGGCGCAAGGTACAGTGGAGGTGGATACGCCCTTCCAA 540
Db 481 CTGAATAACTTTCTATCCCGAGAGGCGCAAGGTACAGTGGAGGTGGATACGCCCTTCCAA 540
Qy 541 TCCGGTTAACTCCCGAGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 600
Db 541 TCCGGTTAACTCCCGAGAGAGTGTACAGAGCAGGAGTGTACAGAGCAGGACAGCACCTACAGCCTC 600
Qy 601 AGCAGCACCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGGGAA 660
Db 601 AGCAGCACCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGGGAA 660
Qy 661 GTCACCCATCAGGGCCTGAGCTCGCCCGTACAAAGAGCTTCAACAGGGGAGAGTGT 718
Db 661 GTCACCCATCAGGGCCTGAGCTCGCCCGTACAAAGAGCTTCAACAGGGGAGAGTGT 718

Search completed: April 5, 2003, 20:19:19
Job time : 198.594 secs

XX PI Yuqiu J, Mitcham JL;
 XX WPI; 2001-041426/05.
 XX PT New polynucleotides encoding breast tumor specific proteins, useful for
 XX prevention, treatment and diagnosis of breast cancer -
 XX Claim 25; Page 135-136; 165pp; English.
 XX The present invention provides the coding sequences for a number of
 CC breast cancer related proteins. These can be used in vaccinations
 CC against, diagnosis of and treatment of cancer, particularly breast
 CC cancer.
 XX Sequence 963 BP; 253 A; 264 C; 224 G; 213 T; 9 other;
 SQ
 Query Match 83.5%; Score 601.2; DB 22; Length 963;
 Best Local Similarity 89.8%; Pred. No. 1.5e-150;
 Matches 645; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 QY 1 ATGAGCCTCCCTGCTCAGCTCCTCGGCTGCTATGCTCTGGTCCCGGGTCAAGTGG 60
 DB |||||
 QY 3 ATGAGCCTCCCTGCTCAGCTCCTCGGCTGCTATGCTCTGGTCTCGATCCAGTGG 62
 DB |||||
 QY 61 GAAGTTGATGATCTAGTCTCCACTGTCCCTTCCCATCACACCTGGAGAGCCGCTCC 120
 DB |||||
 QY 63 GATATTGTGATGATCTAGTCTCCACTCTCCAGCCCGTCACTTGGAGAGCCGCTCC 122
 DB |||||
 QY 121 ATCTCTGTAGTCTAGTCTCAAGCTTAAACACAGTATGAGACACCTTCTGAGTTGG 180
 DB |||||
 QY 123 ATCTCTGCAAGTCTAGTCTCAGAGCTCTACATAGTATGATACAGTATTGGATTGG 182
 DB |||||
 QY 181 TATCAGCAGAGCCAGGCACTCCAGGCTCTGATTTATAGGTTCTTAACCGGAC 240
 DB |||||
 QY 183 TACCTGCAAGCCAGGACAGTCTCCAGCTCTGATTTGGCTTTTACCGGGCC 242
 DB |||||
 QY 241 TCTGGGTCCTCAGACAGATTCAGGCGAGTGGGCGAGGACAGATTTCACTGAAATC 300
 DB |||||
 QY 243 TCGGGGTCCTCAGACAGTTCAGGCGAGTGGGCGAGGACAGATTTTACACTGAGATC 302
 DB |||||
 QY 301 AGCGAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGGGGCAAGGTACAAGGACTCT 360
 DB |||||
 QY 303 AGTAGAGTGGAGGCTGAGGATGTTGGCTTTTATTAATCTCATGCAAACTCTACAGACCCG 362
 DB |||||
 QY 361 CCACATTTTCGGCGGAGGACCAAGGTGGAAATCAAAAGTACGGTGGCTGCACCATCTGTC 420
 DB |||||
 QY 363 CTCACATTTTCGGCGGAGGACCAAGGTGGAGATCAAAAGTGTGGCTGCACCATCTGTC 422
 DB |||||
 QY 421 TTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATGCTCTGTTGTGCTG 480
 DB |||||
 QY 423 TTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATGCTCTGTTGTGCTG 482
 DB |||||
 QY 481 CTGATTAATCTTATCCAGAGGACCAAGTACAGTGAAGTGAATACAGCCCTCCAA 540
 DB |||||
 QY 483 CTGATTAATCTTATCCAGAGGACCAAGTACAGTGAAGTGAATACAGCCCTCCAA 542
 DB |||||
 QY 541 TCGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACTACAGCTC 600
 DB |||||
 QY 543 TCGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACTACAGCTC 602
 DB |||||
 QY 601 AGCAGCACCCTGACGCTGAGCAAGCAGACTACGAGAAACAAAGTCTACGCTCGAA 660
 DB |||||
 QY 603 AGCAGCACCCTGACGCTGAGCAAGCAGACTACGAGAAACAAAGTCTACGCTCGAA 662
 DB |||||
 QY 661 GTACCCATCAGGCGCTGAGCTGCCCGTCAACAGAGCTTCAACAGGGAGAGTGT 718
 DB |||||
 QY 663 GTACCCATCAGGCGCTGAGCTGCCCGTCAACAGAGCTTCAACAGGGAGAGTGT 720
 DB |||||

RESULT 15

AAA13924

ID AAA13924 standard; DNA; 720 BP.

XX AAA13924;
 AC 02-AUG-2000 (first entry)
 DT Human PTHrP monoclonal antibody clone 2F8-10-3 DNA SEQ ID NO:11.
 DE Human PTHrP monoclonal antibody clone 2F8-10-3 DNA SEQ ID NO:11.
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.
 OS Homo sapiens.
 XX JP2000080100-A.
 XX 21-MAR-2000.
 XX 12-OCT-1998; 98JP-0304793.
 XX 17-JUN-1998; 98JP-0188196.
 XX 26-JUN-1998; 98JP-0196729.
 XX (NISR) JAPAN TOBACCO INC.
 PA WPI; 2000-286723/25.
 DR P-PSDB; AAY02614.
 XX A human monoclonal antibody to parathyroid hormone related protein. -
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain
 XX Example 10; Page 41-42; 88pp; Japanese.
 CC The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone nucleotide sequence from the
 CC present invention.
 SQ Sequence 720 BP; 174 A; 190 C; 188 G; 163 T; 5 other;
 Query Match 83.2%; Score 599.4; DB 21; Length 720;
 Best Local Similarity 89.4%; Pred. No. 4e-150;
 Matches 642; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
 QY 1 ATGAGCTCCCTGCTCAGCTCCTCGGCTGCTATGCTCTGCTCCCGGGTCCAGTGG 60
 DB |||||
 QY 1 ATGAGCTCCCTGCTCAGCTCCTCGGCTGCTATGCTCTGCTCCCGGGTCCAGTGG 60
 DB |||||
 QY 61 GAAGTTGATGATGATCTCAGTCTCCACTGTCCCTTCCCATCACCTGGAGAGCCGCTCC 120
 DB |||||
 QY 61 GATATTGTGATGATGATCTCAGTCTCCACTGTCCCTTCCCATCACCTGGAGAGCCGCTCC 120
 DB |||||
 QY 121 ATCTCTGTAGTCTAGTCTCAAGCTTAAACACAGTATGAGACACCTTCTGAGTTGG 180
 DB |||||
 QY 121 ATCTCTGTAGTCTAGTCTCAAGCTTCTGCTATGATGATGATGATGATGATGATG 180
 DB |||||
 QY 181 TATCAGCAGAGCCAGGCACTCCAGGCTCTGATTTATAGGTTCTTAACCGGAC 240
 DB |||||
 QY 181 TACCTGCAAGCCAGGACAGTCTCCAGCTCTGATTTGGCTTTTACCGGGCC 240
 DB |||||
 QY 241 TCTGGGTCCTCAGACAGTTCAGGCGAGTGGGCGAGGACAGATTTTACACTGAGATC 300
 DB |||||


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QY 121 ATCTCTGTAGTCTAGTCAAAAGCCTTAAACACAGTAATGGAGACACCTTCTCGATTGG 180
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 ATCTCTGCAGATCTAGTAAGACCTTGTACACAGTAATGGAAACACCTATTACATTGG 180
QY 181 TATCAGCAGAAGCCAGGCCAACTTCAAGGCTCTGATTATTAAGGTTCTTAACCGGGAC 240
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 TACCTGCAGAAGCCAGGCCAGTCTCAAGGCTCCTGATCTACAAAGTTTCCAACCGATT 240
QY 241 TCTGGGGTCCACACAGATTACGGCAGTGGGAGGAGACAGATTTCACACTGAAAAATC 300
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 TCTGGGGTCCACACAGATTACGGCAGTGGGTGAGGACTGATTTACACTGAAAAATC 300
QY 301 AGCGAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTCGGGCAAGGTACAGGACTCCT 360
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 AGCAGGTTGGAGGCTGAGGATGTTGGGGTTTATTAATCTCTCAAGTACACATGTTCT 360
QY 361 CCACATTTGGGGAGGAGCCAAAGGTGGAATCAAAAGTACGGTGGCTGCACCATCTGTC 420
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
361 CCGGGCTTCGGCCAAAGGACCAAGGTGGAATCAAAAGTACTGTGGCTGCACCATCTGTC 420
QY 421 TTCAATCTCCCGCATCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTGCTG 480
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
421 TTCAATCTCCCGCATCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTGCTG 480
QY 481 CTGAATAACTTCTATCCAGAGAGCCAAAGTACAGTGAAGGTGGAATACCGCTCCAA 540
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CTGAATAACTTCTATCCAGAGAGCCAAAGTACAGTGAAGGTGGAATACCGCTCCAA 540
QY 541 TCGGGTAACCTCCAGGAGAGTGTCAAGAGCGGACAGCAAGGACAGCACTTACAGCTC 600
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
541 TCGGGTAACCTCCAGGAGAGTGTCAAGAGCGGACAGCAAGGACAGCACTTACAGCTC 600
QY 601 AGCAGCAGCTGAGCTGAGCAAGCAGACTAGGAAACACAAAGTCTACCGCTCGGAA 660
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
601 AGCAGCAGCTGAGCTGAGCAAGCAGACTAGGAAACACAAAGTCTACCGCTCGGAA 660
QY 661 GTCAACCATCAGGGCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 718
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
661 GTCAACCATCAGGGCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 718

RESULT 12
AAV61359
ID AAV61359 standard; cDNA to mRNA; 720 Bp.
AC
XX
AC AAV61359;
XX
DT 18-JAN-1999 (first entry)
XX
DE Anti-human Fas humanised antibody CH11 light chain VL-KY cDNA.
XX
KW Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;
KW autoimmune disease; rheumatoid arthritis; therapy; human;
KW antibody engineering; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT sig_peptide 1..60
FT /*tag= a
FT mat_peptide 61..717
FT /*tag= b
XX
XX EP866131-A2.
PN
XX
XX 23-SEP-1998.
XX
XX 20-MAR-1998; 98EP-0302113.
XX
XX 21-MAR-1997; 97JP-0067938.
XX
XX (SANTY ) SANKYO CO LTD.
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XX
PI Haruyama H, Nakahara K, Serizawa N, Takahashi T;
PI Yonehara S;
XX
XX WPI; 1998-482965/42.
DR P-PSDB; AAW71876.
XX
PT Production of anti-Fas protein humanised antibodies - for use in
PT inducing apoptosis on Fas expressing cells in the treatment of
PT autoimmune diseases, especially rheumatoid arthritis
XX
PS Example 3; Page 92-93; 187pp; English.
XX
XX This cDNA sequence codes for a humanised anti-Fas antibody CH11
CC light chain (see AAW71876), designated VL-KY. VL-KY is based on the
CC light chain (see AAW71883) of murine anti-human Fas monoclonal
CC antibody CH11. The humanised sequence was designed following
CC selection of donor residues from CH11 to be grafted onto acceptor
CC molecule RPM1610'CL. 4 Light chain sequences (see AAW71876-79) have
CC been designed, and each can be used in combination with either of 2
CC heavy chain sequences (see AAW71880-81) to provide novel, claimed
CC humanised CH11 IGM antibodies that lack a J chain. These humanised
CC anti-human Fas antibodies are capable of inducing apoptosis in cells
CC expressing Fas (e.g. synoviocytes) and are useful in the treatment
CC of autoimmune disease and chronic rheumatoid arthritis. DNA
CC sequences encoding the humanised antibodies are claimed, as are
CC vectors such as pKappakV2-58 including the VL-KY nucleotide
CC sequence, and host cells such as Escherichia coli pKappakV2-58
CC (FERM BP-5861).
XX
SQ Sequence 720 Bp; 180 A; 200 C; 184 G; 156 T; 0 other;
```

```
Query Match 85.7%; Score 617.2; DB 19; Length 720;
Best Local Similarity 91.2%; Pred. No. 7.2e-155;
Matches 655; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 ATGAGCCTCCCTGCTGCTAGCTCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGG 60
DB 1 ATGAGGCTCCCTGCTGCTAGCTCTCGGGCTGCTAATGCTCTGGGTCCCGAGTCCAGTGG 60
QY 61 GAAGTTGTGATGACTGACTGCTCCACTGCTCCCTTCCCATCACACTGGAGAGCCGGCTCC 120
DB 61 GATGTTGTGATGACTGACTGCTCCACTGCTCCCTTCCCATCACACTGGAGAGCCGGCTCC 120
QY 121 ATCTCTCTGATGCTAGTCAAAAGCCTTAAACACAGTAATGGAGACACTTCTCTGAGTTGG 180
DB 121 ATCTCTCGAGATCTAGTAGAGCCTTGTACACAGTAATGGAAACACCTATTACATTGG 180
QY 181 TATCAGCAGAAGCCAGGCCAACTTCAAGGCTCCTGATTTATTAAGGTTTCTAACCGGGAC 240
DB 181 TACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCGATT 240
QY 241 TCTGGGTCCACACAGATTACGGCGCAGTGGGGCAGGACAGATTTCACACTGAAAAATC 300
DB 241 TCTGGGTCCACACAGATTACGGCGCAGTGGGTTCAGGCACTGATTTTCACACTGAAAAATC 300
QY 301 AGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTCGGGCAAGGTACAAAGACTCCT 360
DB 301 AGCAGGTTGGAGGCTGAGGATGTTGGGGTTTATTAATCTCTCAAGTACACATGTTCT 360
QY 361 CCCACTTTCCGGCGGAGGACCAAGGTGGAATCAAAAGTACGGTGGCTGCACCATCTGTC 420
DB 361 CCGGGTTCGGCCAAAGGACCAAGGTGGAATCAAAAGTACTGTGGGTGCACCATCTGTC 420
QY 421 TTCAATCTCCCGCATCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTGCTG 480
DB 421 TTCAATCTCCCGCATCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTGCTG 480
QY 481 CTGAATAACTTCTATCCAGAGAGCCAAAGTACAGTGAAGGTGGAATACCGCTCCAA 540
DB 481 CTGAATAACTTCTATCCAGAGAGCCAAAGTACAGTGAAGGTGGAATACCGCTCCAA 540
QY 541 TCGGGTAACCTCCAGGAGAGTGTCAAGAGCAGGACAGCAAGGACAGCACTTACAGCTC 600
```

CC The present invention relates to antirheumatic agents which comprise as
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein
CC does not include a J segment, has apoptosis inducing activity, and
CC consists of a light and heavy chain polypeptide produced synthetically.
CC The agents of the invention exhibit antirheumatic and immunosuppressive
CC activity and can be used to treat autoimmune diseases, especially
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen
CC binding properties. Included in the invention are nucleotide sequences
CC of the IgM light and heavy chains (see AAB12902-B12907) and the
CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and
CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see
CC AAB12902-A78266) and protein sequences (see AAB12908-B12910). Also
CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).
CC Primers specific for the anti-human Fas antibody, light, heavy and kappa
CC chains used in the invention are represented by sequences
CC AAB12913-A78266. Primers used for sequencing the human Ig DNA used in the
CC invention are represented by sequences AAB12913-A78266 and
CC AAB12913-A78266, while humanised anti-Fas Ig DNA sequencing primers are
CC represented by sequences AAB12913-A78266 and AAB12913-A78266. Primer
CC sequences AAB12913-A78266 are specific for murine Ig DNA, and are used in
CC the production of the agent of the invention.

XX SQ Sequence 720 BP; 179 A; 200 C; 184 G; 157 T; 0 other;

Query Match 85.9%; Score 618.8; DB 21; Length 720;
Best Local Similarity 91.4%; Pred. No. 2.7e-155;
Matches 656; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATGCTCTGCGTCCCGGGTCCAGTGGG 60
DB 1 ATGAGGCTCCCTGCTCAGCTCCTCGGGCTGCTATGCTCTGCGTCCCGGGTCCAGTGGG 60
QY 61 GAAGTTGTGATGACTCAGTCTCAGTCTCCACTTCCCTGCGGCTCAGTCTCCAGTCTCC 120
DB 61 GATGTTGTGATGACTCAGTCTCAGTCTCCACTTCCCTGCGGCTCAGTCTCCAGTCTCC 120
QY 121 ATCTCTGTAGTCTAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAG 180
DB 121 ATCTCTGTAGTCTAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAG 180
QY 181 TATCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
DB 181 TACCTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY 241 TCTGGGCTCCAGACAGATTCAGGCGAGTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB 241 TCTGGGCTCCAGACAGATTCAGGCGAGTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 301 AGCGCAGTGGAGGCTGAAGATGTTGGGTTTATTTCTGCGGGCAAGGTACAGGACTCCT 360
DB 301 AGCAGGTGGAGGCTGAGGATGTTGGGTTTATTTCTGCTCTCAAAGTACACATGTTCTCT 360
QY 361 CCCACTTTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
DB 361 CCGGCGTTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 421 TCCATCTTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
DB 421 TCCATCTTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 481 CTGAATAACTTCTATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB 481 CTGAATAACTTCTATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 TCGGGTAACTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
DB 541 TCGGGTAACTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
QY 601 AGCAGCAGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
DB 601 AGCAGCAGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 661 GTCAACCATCAGGCGCTGAGTCTGCGCGCTCACAAGAGCTTCAACAGGGGAGGAGTGT 718

DB 661 GTCAACCATCAGGCGCTGAGTCTGCGCGCTCACAAGAGCTTCAACAGGGGAGGAGTGT 718

RESULT 11

AAA78269
ID AAA78269 standard; DNA; 720 BP.
XX AAA78269;
AC AAA78269;
XX
DT 16-NOV-2000 (first entry)

DE Anti-human Fas immunoglobulin M light chain DNA sequence SEQ ID #81.
KW Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
KW immunosuppression; autoimmune disease; treatment; rheumatism;
KW anti-Fas antibody; ss.
OS Synthetic.

XX JP2000154149-A.
XX
XX 06-JUN-2000.
XX
XX 17-SEP-1999; 99JP-0263984.
XX
XX 18-SEP-1998; 98JP-0264598.
XX

PA (SANY) SANKYO CO LTD.

DR WPI; 2000-454476/40.

DR P-PSDB; AAB12915.

PT Anti-human Fas humanizing antibody-containing antirheumatic agents -

XX Example 2; Page 69-70; 109pp; Japanese.

CC The present invention relates to antirheumatic agents which comprise as
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein
CC does not include a J segment, has apoptosis inducing activity, and
CC consists of a light and heavy chain polypeptide produced synthetically.
CC The agents of the invention exhibit antirheumatic and immunosuppressive
CC activity and can be used to treat autoimmune diseases, especially
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen
CC binding properties. Included in the invention are nucleotide sequences
CC of the IgM light and heavy chains (see AAB12913-B12918 and AAB12919), and
CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and
CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see
CC AAB12902-A78266) and protein sequences (see AAB12908-B12910). Also
CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).
CC Primers specific for the anti-human Fas antibody, light, heavy and kappa
CC chains used in the invention are represented by sequences
CC AAB12913-A78266. Primers used for sequencing the human Ig DNA used in the
CC invention are represented by sequences AAB12913-A78266 and
CC AAB12913-A78266, while humanised anti-Fas Ig DNA sequencing primers are
CC represented by sequences AAB12913-A78266 and AAB12913-A78266. Primer
CC sequences AAB12913-A78266 are specific for murine Ig DNA, and are used in
CC the production of the agent of the invention.

XX SQ Sequence 720 BP; 179 A; 200 C; 185 G; 156 T; 0 other;

Query Match 85.9%; Score 618.8; DB 21; Length 720;
Best Local Similarity 91.4%; Pred. No. 2.7e-155;
Matches 656; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATGCTCTGCGTCCCGGGTCCAGTGGG 60
DB 1 ATGAGGCTCCCTGCTCAGCTCCTCGGGCTGCTATGCTCTGCGTCCCGGGTCCAGTGGG 60
QY 61 GAAGTTGTGATGACTCAGTCTCAGTCTCCACTTCCCTGCGGCTCAGTCTCCAGTCTCC 120
DB 61 GATGTTGTGATGACTCAGTCTCAGTCTCCACTTCCCTGCGGCTCAGTCTCCAGTCTCC 120

AC AAV61361;
 XX 18-JAN-1999 (first entry)
 DE Anti-human Fas humanised antibody CH11 light chain VL-RY cDNA.
 XX Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;
 KW autoimmune disease; rheumatoid arthritis; therapy; human;
 KW antibody engineering; ds.
 KW Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH sig_peptide 1..60
 FT /tag= a
 FT mat_peptide 61..717 b
 FT /tag= b
 XX
 PN EP866131-A2.
 XX
 XX 23-SEP-1998.
 XX
 PF 20-MAR-1998; 98EP-0302113.
 XX
 PR 21-MAR-1997; 97JP-0067938.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Haruyama H, Nakahara K, Serizawa N, Takahashi T;
 PI Yonehara S;
 XX
 DR WPI; 1998-482965/42.
 DR P-PSDB; AAW71878.
 XX
 XX Production of anti-Fas protein humanised antibodies - for use in
 PT inducing apoptosis on Fas expressing cells in the treatment of
 PT autoimmune diseases, especially rheumatoid arthritis
 PS Example 3; Page 97-98; 187pp; English.
 XX
 CC This cDNA sequence codes for a humanised anti-Fas antibody CH11
 CC light chain (see AAW71878), designated VL-RY. VL-RY is based on the
 CC light chain (see AAW71889) of murine anti-human Fas monoclonal
 CC antibody CH11. The humanised sequence was designed following
 CC selection of donor residues from CH11 to be grafted onto acceptor
 CC molecule RPM16410'CL. 4 Light chain sequences (see AAW71876-79) have
 CC been designed, and each can be used in combination with either of 2
 CC heavy chain sequences (see AAW71880-81) to provide novel, claimed
 CC humanised CH11 IgM antibodies that lack a J chain. These humanised
 CC anti-human Fas antibodies are capable of inducing apoptosis in cells
 CC expressing Fas (e.g. synovocytes) and are useful in the treatment
 CC of autoimmune disease and chronic rheumatoid arthritis. DNA
 CC sequences encoding the humanised antibodies are claimed, as are
 CC vectors such as pPKappary2-10 including the VL-RY nucleotide
 CC sequence, and host cells such as Escherichia coli pPKappary2-10
 CC (PERM BP-5859).
 XX
 SQ Sequence 720 BP; 179 A; 200 C; 185 G; 156 T; 0 other;

Query Match 85.9%; Score 618.8; DB 19; Length 720;
 Best Local Similarity 91.4%; Pred. No. 2.7e-155;
 Matches 656; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 ATGAGGCTCCCTGCTAGCTCCCTGGGCTGCTATTGCTGCTGCTCCCGGCTCCAGTGGG 60
 DB |||||
 QY 1 ATGAGGCTCCCTGCTAGCTCCCTGGGCTGCTATTGCTGCTGCTCCCGGCTCCAGTGGG 60
 DB |||||
 QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACACTCCAGAGCGGGCTCC 120
 DB |||||
 QY 61 GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTTGACAGCGGGCTCC 120
 DB |||||
 QY 121 ATCTCCTGTAGGCTAGTCAAGCCTTAAACACAGTAATGGAGACACTTCTCTGAGTTGG 180

DB 121 ATCTCCTGTAGTCTAGTAAAGGCTTGTACAGTAATGGAACACCTATTATACATGG 180
 QY 181 TATCAGCAGAAAGCAGGCCAACCTTCAAGGCTCTGATTTATTAAGGTTTCTAAACCGGAC 240
 DB 181 TACCTGCAGAAAGCAGGCCAGTCTTCAAGGCTCTGATCTACAAAGTTTCCAAACCGATT 240
 QY 241 TCTGGGTTCCAGACAGATTTCAGGGCAGTGGGCGAGGACAGATTTTCACACTGAAATC 300
 DB 241 TCTGGGTTCCAGACAGATTTCAGGGCAGTGGGTCAGGCACTGATTTTCACACTGAAATC 300
 QY 301 AGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGCGGGCAAGGTACAAGGACTCCT 360
 DB 301 AGCAGGTTGGAGGCTGAGGATGTTGGGGTTTATTTACTGCTCTCAAAGTACACATGTTCT 360
 QY 361 CCCACTTTCCGGCGGAGGACCAAGGTGGAATCAAACTACGTCGGTGGTGCACCACTCTGTC 420
 DB 361 CCGCGTTTCGGCCCAAGGACCAAGGTGGAATCAAACTACTGTGGCTGCACCACTCTGTC 420
 QY 421 TTCATCTTCCCGCCATCTGATGACAGTGAATCTGGAATCTGCTCTGTTGTGCTG 480
 DB 421 TTCATCTTCCCGCCATCTGATGACAGTGAATCTGGAATCTGCTCTGTTGTGCTG 480
 QY 481 CTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCTCCAA 540
 DB 481 CTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCTCCAA 540
 QY 541 TCGGGTAATCCAGAGAGTGTCTACAGAGCAGACAGCAGAGCAGCAGCCTACAGCCTC 600
 DB 541 TCGGGTAATCCAGAGAGTGTCTACAGAGCAGACAGCAGAGCAGCAGCCTACAGCCTC 600
 QY 601 AGCAGACCTCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGGAA 660
 DB 601 AGCAGACCTCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGGAA 660
 QY 661 CTCACCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGAGAGTGT 718
 DB 661 CTCACCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGAGAGTGT 718

RESULT 10
 AAA78268
 ID AAA78268 standard; DNA; 720 BP.
 AC AAW78268;
 XX 16-NOV-2000 (first entry)
 DT Anti-human Fas immunoglobulin M light chain DNA sequence SEQ ID #79.
 DE Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
 KW immunosuppression; autoimmune disease; treatment; rheumatism;
 KW anti-Fas antibody; ss.
 XX Synthetic.
 OS
 XX JP2000154149-A.
 PN 06-JUN-2000.
 PD 17-SEP-1999; 99JP-0263984.
 PF 18-SEP-1998; 98JP-0264598.
 PR (SANY) SANKYO CO LTD.
 XX WPI; 2000-454476/40.
 DR P-PSDB; AAB12914.
 XX
 PT Anti-human Fas humanizing antibody-containing antirheumatic agents -
 PS Example 2; Page 67-68; 109pp; Japanese.
 XX

QY 361 CCACATTTGGCGGAGGACCAAGGTGGAAATCAAACTACGGTGGCTGCACCATCTGTC 420
DB 401 TGGACGCTTGGCCCAAGGAGCGAAGGTGGAAACCAAAACGAACTGTGGCTGCACCATCTGTC 460
QY 421 TTCACTTTCCTCCGCACTGTATGAGCAGTGTGAATCTGGAACTGCCTCTCTGTGTGTCCTG 480
DB 461 TTCACTTTCCTCCGCACTGTATGAGCAGTGTGAATCTGGAACTGCCTCTCTGTGTGTCCTG 520
QY 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGAAAGTGGATTAACGCCCTCCAA 540
DB 521 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGAAAGTGGATTAACGCCCTCCAA 580
QY 541 TCGGTTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGAGACGACCTACAGCCTC 600
DB 581 TCGGTTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGAGACGACCTACAGCCTC 640
QY 601 AGCAGCAGCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCCTCGAA 660
DB 641 AGCAGCAGCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCCTCGAA 700
QY 661 GTCAACCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 718
DB 701 GTCAACCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 758

RESULT 8
AAV61360
ID AAV61360 standard; cDNA to mRNA; 720 BP.
AC AAV61360;
XX

18-JAN-1999 (first entry)
XX Anti-human Fas humanised antibody CH11 light chain VL-KF cDNA.
XX Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;
KW autoimmune disease; rheumatoid arthritis; therapy; human;
XX antibody engineering; ds.
OS Homo sapiens.
OS Synthetic.

Key Location/Qualifiers
FT sig_peptide 1..60
FT mat_peptide 61..717
FT /*tag= a
FT /*tag= b
XX EP866131-A2.
XX 23-SEP-1998.
XX 20-MAR-1998; 98EP-0302113.
XX 21-MAR-1997; 97JP-0067938.
XX (SANY) SANKYO CO LTD.
XX Haruyama H, Nakahara K, Serizawa N, Takahashi T;
XX Yonehara S;
XX WPI; 1998-482965/42.
DR P-PSDB; AAW71877.
XX

Production of anti-Fas protein humanised antibodies - for use in
PT inducing apoptosis on Fas expressing cells in the treatment of
PT autoimmune diseases, especially rheumatoid arthritis
XX
XX Example 3; Page 95-96; 187pp; English.
PS
XX

This cDNA sequence codes for a humanised anti-Fas antibody CH11
CC light chain (see AAW71877), designated VL-KF. VL-KF is based on the
CC light chain (see AAW71889) of murine anti-human Fas monoclonal
CC

CC antibody CH11. The humanised sequence was designed following
CC selection of donor residues from CH11 to be grafted onto acceptor
CC molecule RPI6410'Cl. 4 light chain sequences (see AAW71876-79) have
CC been designed, and each can be used in combination with either of 2
CC heavy chain sequences (see AAW71880-81) to provide novel, claimed
CC humanised CH11 IGM antibodies that lack a J chain. These humanised
CC anti-human Fas antibodies are capable of inducing apoptosis in cells
CC expressing Fas (e.g. synovocytes) and are useful in the treatment
CC of autoimmune disease and chronic rheumatoid arthritis. DNA
CC sequences encoding the humanised antibodies are claimed, as are
CC vectors such as pKappaKF2-19 including the VL-KF nucleotide
CC sequence, and host cells such as Escherichia coli pKappaKF2-19
CC (FERM BP-5860).
XX
SQ Sequence 720 BP; 179 A; 200 C; 184 G; 157 T; 0 other;

Query Match 85.9%; Score 618.8; DB 19; Length 720;
Best Local Similarity 91.4%; Pred. No. 2.7e-155;
Matches 656; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 ATGAGCCTCCTGCTCAGCTCTCGGCTGCTATTTGCTCTCGGTCCTCCGGTCCAGTGGG 60
DB 1 ATGAGCCTCCTGCTCAGCTCTCGGCTGCTATTTGCTCTCGGTCCTCCAGTCCAGTGGG 60
QY 61 GAAGTTGTGATGACTCAGTCTCCACTGCTCCCTTCCCATCACCTGAGAGCGCGCTCC 120
DB 61 GATGTTGTGATGACTCAGTCTCCACTGCTCCCTTCCCATCACCTGAGAGCGCGCTCC 120
QY 121 ATCTCTGTAGTCTAGTCAAGGCTTTAAACACAGTAATGAGACACCTTCTCTGAGTTGG 180
DB 121 ATCTCTGTAGTCTAGTCAAGGCTTTAAACACAGTAATGAGACACCTTCTCTGAGTTGG 180
QY 181 TATCAGCAGAAAGCCAGGCCAACCTCCAAAGCTCTCTGATTTATTAAGGTTTCTAACCGGAC 240
DB 181 TACCTGAGAAAGCCAGGCCAGTCTCTCAAGCTCTCTGATTTATTAAGGTTTCTAACCGGAT 240
QY 241 TCTGGGTCCTCAGACAGATTCAGCGGCGAGTGGGCGAGGACAGATTTTCAACATGAAATC 300
DB 241 TCTGGGTCCTCAGACAGATTCAGCGGCGAGTGGGCGAGGACAGATTTTCAACATGAAATC 300
QY 301 AGCGCAGTGGAGGCTGAAGATGTTGGGCTTTATTTCTCGGGCAAGGTACAGGACTCCT 360
DB 301 AGCGGAGTGGAGGCTGAGGATGTTGGGCTTTATTTCTGCTCTCAAGTACACATGTTCT 360
QY 361 CCCACTTTTCGGCGGAGGACCAAGTGGAAATCAAAAGTACGCTGCTGACCAATCTGTC 420
DB 361 CCGGCTTTCGGCGGAGGACCAAGTGGAAATCAAAAGTACGCTGCTGCTGACCAATCTGTC 420
QY 421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTGTTGTGCTG 480
DB 421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTGTTGTGCTG 480
QY 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGAAAGTGGATTAACGCCCTCCAA 540
DB 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGAAAGTGGATTAACGCCCTCCAA 540
QY 541 TCGGTTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGAGACGACCTACAGCCTC 600
DB 541 TCGGTTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGAGACGACCTACAGCCTC 600
QY 601 AGCAGCAGCTGAGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCCTCGAA 660
DB 601 AGCAGCAGCTGAGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCCTCGAA 660
QY 661 GTCAACCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 718
DB 661 GTCAACCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 718

RESULT 9
AAV61361
ID AAV61361 standard; cDNA to mRNA; 720 BP.
XX

CC antibodies comprising humanised light and heavy chains (see
 CC AAW71876-81) derived from the murine anti-human Fas monoclonal
 CC antibody CH11. The humanised anti-human Fas antibodies are
 CC capable of inducing apoptosis in cells expressing Fas (e.g.
 CC synovialocytes) and are useful in the treatment of autoimmune disease
 CC and chronic rheumatoid arthritis.
 XX

Sequence 891 BP; 204 A; 267 C; 225 G; 195 T; 0 other;

Query Match 86.2%; Score 620.4; DB 19; Length 891;
 Best Local Similarity 91.5%; Pred. No. 1.1e-155;
 Matches 657; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 ATGAGCCTCCCTGCTCAGCTCTCGGGCTGCTATTGCTCTCGTCCCGGGTCCAGTGGG 60
 DB 41 ATGAGGCTCCCTGCTCAGCTCTCGGGCTGCTAATGCTCTGGTCCAGGATCCAGTGGG 100

QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCTCCCTGCGCTGACAGCGGCTCC 120
 DB 101 GATGTTGTGATGACTCAGTCTCCACTGTCCTCCCTGCGCTGACAGCGGCTCC 160

QY 121 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAAATGAGGATTTCTAGATTGG 180
 DB 161 ATCTCTGAGCTCTAGTCAAGCCTTAAACACAGTAAATGAGGATTTCTAGATTGG 220

QY 181 TATCAGCAGAGCCAGGCGCAACCTCCAAGGCTTAAATGAGGATTTCTAGATTGG 240
 DB 221 TTTTCATCAGAGCCAGGCGCAACCTCCAAGGCTTAAATGAGGATTTCTAGATTGG 280

QY 241 TCTGGGTTCCAGCAGATTTACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 281 TCTGGGTTCCAGCAGATTTACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 340

QY 301 AGCGCAGTGGAGGCTCAAGATGTTGGGGTATTATTTCTGGGCGAAGGTACAGGACTCCT 360
 DB 341 AGCAGGGTGGAGGCTGAGGATGTTGGGGTATTATTTCTGGGCGAAGGTACAGGACTCCT 400

QY 361 CCCACTTTTCGGCGGAGGACCAAGGTGGAATCAACGTAAGTGGCTGCACTCTGTC 420
 DB 401 TGGAGCTTTCGGCGGAGGACCAAGGTGGAATCAACGTAAGTGGCTGCACTCTGTC 460

QY 421 TTTCATCTTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTGCTGCTGCTG 480
 DB 461 TTTCATCTTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTGCTGCTGCTG 520

QY 481 CTGATAACTTCTATCCAGAGAGCCAAAGTACAGTGGAAAGTGGATAAGCCCTCCAA 540
 DB 521 CTGATAACTTCTATCCAGAGAGCCAAAGTACAGTGGAAAGTGGATAAGCCCTCCAA 580

QY 541 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 600
 DB 581 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 640

QY 601 AGCAGCAGCCTGAGCTGAGCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 660
 DB 641 AGCAGCAGCCTGAGCTGAGCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 700

QY 661 GTCAACCATCAGGCGCTGAGCTGCGCGCTGCAAGAGCTTTCAACAGGGAGAGTGT 718
 DB 701 GTCAACCATCAGGCGCTGAGCTGCGCGCTGCAAGAGCTTTCAACAGGGAGAGTGT 758

RESULT 7
 AAA78320
 ID AAA78320 standard; DNA; 891 BP.
 XX
 AC AAA78320;
 XX
 DT 16-NOV-2000 (first entry)
 XX
 DE Anti-human Fas Ig CH11 nucleotide SEQ ID #138.
 XX
 KW Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;

KW immunosuppression; autoimmune disease; treatment; rheumatism;
 KW anti-Fas antibody; ss.

OS Homo sapiens.

PN JP2000154149-A.

XX 06-JUN-2000.

XX 17-SEP-1999; 99JP-0263984.

XX 18-SEP-1998; 98JP-0264598.

XX (SANY) SANKYO CO LTD.

XX WPI; 2000-454476/40.

XX Anti-human Fas humanizing antibody-containing antirheumatic agents -

Example 5; Page 92; 109pp; Japanese.

XX The present invention relates to antirheumatic agents which comprise as
 CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein
 CC does not include a J segment, has apoptosis inducing activity, and
 CC consists of a light and heavy chain polypeptide produced synthetically.
 CC The agents of the invention exhibit antirheumatic and immunosuppressive
 CC activity and can be used to treat autoimmune diseases, especially
 CC rheumatism. The IgM molecule used in the invention has human Fas-antigen
 CC binding properties. Included in the invention are nucleotide sequences
 CC of the IgM light and heavy chains (see AAW78267-A78272) and the
 CC corresponding protein sequences (see AAW12913-B12918 and AAW12919), and
 CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see
 CC AAW78202-A78206) and protein sequences (see AAW12908-B12910). Also
 CC included are anti-human Fas antibody CDR peptides (AAW12902-B12907).
 CC Primers specific for the anti-human Fas antibody, light, heavy and kappa
 CC chains used in the invention are represented by sequences
 CC AAW78213-A78266. Primers used for sequencing the human Ig DNA used in the
 CC invention are represented by sequences AAW78277-A78318 and
 CC AAW78335-A78337, while humanised anti-Fas Ig DNA sequencing primers are
 CC represented by sequences AAW78321-A78334 and AAW78338-A78367. Primer
 CC sequences AAW78207-A78212 are specific for murine Ig DNA, and are used in
 CC the production of the agent of the invention.

XX Sequence 891 BP; 204 A; 267 C; 225 G; 195 T; 0 other;

Query Match 86.2%; Score 620.4; DB 21; Length 891;
 Best Local Similarity 91.5%; Pred. No. 1.1e-155;
 Matches 657; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 ATGAGCCTCCCTGCTCAGCTCTCGGGCTGCTATTGCTCTCGTCCCGGGTCCAGTGGG 60
 DB 41 ATGAGGCTCCCTGCTCAGCTCTCGGGCTGCTAATGCTCTGGTCCAGGATCCAGTGGG 100

QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCTTCCATCACACCTGGAGAGCGGCTCC 120
 DB 101 GATGTTGTGATGACTCAGTCTCCACTGTCCTTCCATCACACCTGGAGAGCGGCTCC 160

QY 121 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAAATGAGGATTTCTAGATTGG 180
 DB 161 ATCTCTGAGCTCTAGTCAAGCCTTAAATGAGGATTTCTAGATTGG 220

QY 181 TATCAGCAGAGCCAGGCGCAACCTCCAAGGCTTCTGATTATTAAGGTTTCTAACCGGAC 240
 DB 221 TTTTCATCAGAGCCAGGCGCAACCTCCAAGGCTTCTGATTATTAAGGTTTCTAACCGGAC 280

QY 241 TCTGGGTTCCAGCAGATTTACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 281 TCTGGGTTCCAGCAGATTTACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 340

QY 301 AGCGCAGTGGAGGCTGAAAGATGTTGGGGTATTATTTCTGGGCGAAGGTACAGGACTCCT 360
 DB 341 AGCAGGGTGGAGGCTGAGGATGTTGGGGTATTATTTCTGGGCGAAGGTACAGGACTCCT 400

Db 361 CCCACTTTCGGCGGAGCACCAAGGTGGAATCAAAAGCTACGGTGGCTGCACCATCTGTC 420
Qy 421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGGTCTGTTGTGTGCTG 480
Db 421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGGTCTGTTGTGTGCTG 480
Qy 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGGAAGTGGATACGCGCTCCAA 540
Db 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGGAAGTGGATACGCGCTCCAA 540
Qy 541 TCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC 600
Db 541 TCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC 600
Qy 601 AGCAGCACCTCGCTGAGCTGACCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGAA 660
Db 601 AGCAGCACCTCGCTGAGCTGACCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGAA 660
Qy 661 GTCAACCATCAGGGCCTGAGCTGCGCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTGA 720
Db 661 GTCAACCATCAGGGCCTGAGCTGCGCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTGA 720

RESULT 4
AAV61362
ID AAV61362 standard; cDNA to mRNA; 720 BP.

AC AAV61362;
XX
DT 18-JAN-1999 (first entry)
XX Anti-human Fas humanised antibody CH11 VL-RF light chain cDNA.
DE
DE Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;
KW autoimmune disease; rheumatoid arthritis; therapy; human;
KW antibody engineering; ds.
XX
OS Homo sapiens.
OS Synthetic.

PH Key Location/Qualifiers
FT sig_peptide 1..60
FT mat_peptide 61..717
FT /*tag= a
FT /*tag= b
XX
PN EP866131-A2.
XX
XX 23-SEP-1998.
XX 20-MAR-1998; 98EP-0302113.
XX
XX 21-MAR-1997; 97JP-0067938.
XX
XX (SANY) SANKYO CO LTD.
XX Haruyama H, Nakahara K, Serizawa N, Takahashi T;
PI Yonehara S;
XX
XX WPI; 1998-482965/42.
DR P-PSDB; AAW71879.

XX
XX Production of anti-Fas protein humanised antibodies - for use in
PT inducing apoptosis on Fas expressing cells in the treatment of
PT autoimmune diseases, especially rheumatoid arthritis
XX
XX Example 3; Page 100-101; 187pp; English.
XX
XX This cDNA sequence codes for a humanised anti-Fas antibody CH11
CC light chain (see AAW71879), designated VL-RF. VL-RF is based on the
CC light chain (see AAW71889) of murine anti-human Fas monoclonal
CC antibody CH11. The humanised sequence was designed following

CC selection of donor residues from CH11 to be grafted onto acceptor
CC molecule RPM16410/Cl. 4 Light chain sequences (see AAW71876-79) have
CC been designed, and each can be used in combination with either of 2
CC heavy chain sequences (see AAW71880-81) to provide novel, claimed
CC humanised CH11 IgM antibodies that lack a J chain. These humanised
CC anti-human Fas antibodies are capable of inducing apoptosis in cells
CC expressing Fas (e.g. synovialocytes) and are useful in the treatment
CC of autoimmune disease and chronic rheumatoid arthritis. DNA
CC sequences encoding the humanised antibodies are claimed, as are
CC vectors such as pKappapRF2-52 including the VL-RF nucleotide
CC sequence, and host cells such as Escherichia coli pKappapRF2-52
XX (FERM BP-5862).

SQ Sequence 720 BP; 177 A; 200 C; 186 G; 157 T; 0 other;

Query Match 86.4%; Score 622; DB 19; Length 720;
Best Local Similarity 91.6%; Pred. No. 3.8e-156;
Matches 658; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGTCAGGTGG 60
Db 1 ATGAGGCTCCCTGCTCAGCTCCTCGGGCTGCTAATGCTCTGCGTCCCGGTCAGGTGG 60
Qy 61 GAAAGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACCTGGAGAGCCGCTCC 120
Db 61 GATGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACCTGGAGAGCCGCTCC 120
Qy 121 ATCTCCTGTAGTCTAGTCAAGGCTTAAACACAGTAAATGGAGACACTTCTGAGTTGG 180
Db 121 ATCTCCTGCAGATCTAGTAAGAGGCTTGTACACAGTAAATGGAAACACTATTACATTGG 180
Qy 181 TATCAGCAGAGCCAGGCGCAACCTCCAAAGCTCCTGATTTATATAGGTTTCTAACCGGAC 240
Db 181 TACTGTCAGAGCCAGGCGCAAGCTCCCAAGGCTCTGATCTACAAAGTTTCCAAACCGATT 240
Qy 241 TCTGGGTCCAGACAGATTTCAGCGCAGTGGGCGAGGACAGATTTTACACTGAAATC 300
Db 241 TCTGGGTCCAGACAGATTTCAGCGCAGTGGGTCAGGCACTGATTTACACTGAAATC 300
Qy 301 AGCGAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGCGGGCAAGGTACAAGACTCCT 360
Db 301 AGCAGGGTGGAGGCTGAGGATGTTGGGGTTTATTTCTGCTCTCAAAGTACACATGTTCT 360
Qy 361 CCCATTTTCGGCGGAGGAGCCAAAGTGGAAATCAAACTACGCTGCGTGCACCATCTGTC 420
Db 361 CCGGGTTTCGGCCAAAGGACCAAGTGGAAATCAAACTACTGTGGCTGCACCATCTGTC 420
Qy 421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTTGTGTGCTG 480
Db 421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTTGTGTGCTG 480
Qy 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGGAAGTGGATACGCGCTCAA 540
Db 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGGAAGTGGATACGCGCTCAA 540
Qy 541 TCGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC 600
Db 541 TCGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC 600
Qy 601 AGCAGCACCTCGCTGAGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGAA 660
Db 601 AGCAGCACCTCGCTGAGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGAA 660
Qy 661 GTCAACCATCAGGGCCTGAGCTGCGCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 718
Db 661 GTCAACCATCAGGGCCTGAGCTGCGCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 718

RESULT 5
AAA78270
ID AAA78270 standard; DNA; 720 BP.
XX
AC AAA78270;

CC rejection of transplanted organ or tissue for treating proliferative
CC and hyperproliferative diseases, for treating reversible obstructive
CC airways disease, intestinal inflammations and allergies e.g. Crohn's
CC disease and ulcerative colitis, food-related allergies e.g. migraine,
CC rhinitis and eczema, and other types of allergies. The present nucleic
CC acid sequence encodes the light chain of 7B6, a primatised antibody
CC used in the invention to induce apoptosis.

XX
SQ Sequence 720 BP; 178 A; 200 C; 193 G; 149 T; 0 other;

Query Match 100.0%; Score 720; DB 24; Length 720;
Best Local Similarity 100.0%; Pred. No. 2.7e-182; Indels 0; Gaps 0;
Matches 720; Conservative 0; Mismatches 0;

QY 1 ATGAGCCTCCCTCTCAGCTCTCCGCGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60
DB 1 ATGAGCCTCCCTCTCAGCTCTCCGCGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60

QY 61 GAAGTTGTGATGACTCAGTCTCCATGCTCCCTTCCCATCACCTGGAGCGCGCTCC 120
DB 61 GAAGTTGTGATGACTCAGTCTCCATGCTCCCTTCCCATCACCTGGAGCGCGCTCC 120

QY 121 ATCTCTGTAGGCTAGTCAAGCCTTAACACAGTAATGGAGACACCTTCTGAGTTGG 180
DB 121 ATCTCTGTAGGCTAGTCAAGCCTTAACACAGTAATGGAGACACCTTCTGAGTTGG 180

QY 181 TATCAGCAGAGCGAGCCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240
DB 181 TATCAGCAGAGCGAGCCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240

QY 241 TCTGGGTCCCAACAGATTCAGCGCAGTGGGCGAGGACAGATTTACACTGAAATC 300
DB 241 TCTGGGTCCCAACAGATTCAGCGCAGTGGGCGAGGACAGATTTACACTGAAATC 300

QY 301 AGCGCAGTGGAGGCTGAGTGTGGGGTTTATTCTCGGGCAAGGTACAAGGACTCCT 360
DB 301 AGCGCAGTGGAGGCTGAGTGTGGGGTTTATTCTCGGGCAAGGTACAAGGACTCCT 360

QY 361 CCCACTTTCCGGCGAGGGACCAAGGTGGAATCAAACTGAGTGAAGTGAACGCCCTCCAA 540
DB 361 CCCACTTTCCGGCGAGGGACCAAGGTGGAATCAAACTGAGTGAAGTGAACGCCCTCCAA 540

QY 421 TTCAATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAACCTGCTCTGTTGTGCGCTG 480
DB 421 TTCAATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAACCTGCTCTGTTGTGCGCTG 480

QY 481 CTGAATTAACCTTCTATCCAGAGAGGCCAAAGTACAGTGAAGTGAATCAACGCCCTCCAA 540
DB 481 CTGAATTAACCTTCTATCCAGAGAGGCCAAAGTACAGTGAAGTGAATCAACGCCCTCCAA 540

QY 541 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 600
DB 541 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 600

QY 601 AGCAGCACTCTGACGCTGACAAAGCAGACTACGAGAAACACAAAGTCTACGCTCGGAA 660
DB 601 AGCAGCACTCTGACGCTGACAAAGCAGACTACGAGAAACACAAAGTCTACGCTCGGAA 660

QY 661 GTCAACCATCAGGCGCTGAGCTCGCGCTCACAAAGAGCTTCAACAGGGGAGAGTGTGA 720
DB 661 GTCAACCATCAGGCGCTGAGCTCGCGCTCACAAAGAGCTTCAACAGGGGAGAGTGTGA 720

RESULT 3
ID AAT62511 standard; DNA; 720 BP.
XX AAT62511;
AC AAT62511;
XX
DT 25-MAY-1997 (first entry)
XX
DE Primatised anti-human B7.1 antigen antibody 7B6 light chain DNA.
XX

KW Monoclonal antibody; cynomolgus monkey; macaque; 7B6;
KW primatised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma; ss.
XX
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX
PN WO9640878-A1.
XX 19-DEC-1996.
PD
XX 06-JUN-1996; 96WO-US10053.
XX
XX 07-JUN-1995; 95US-0487550.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX
XX WPI: 1997-108638/10.
XX P-PSDB; AAW01819.
XX
XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
XX useful for treating autoimmune disease or graft-versus-host disease
XX
XX Claim 9; Fig 9A; 81pp; English.
XX
XX 2 DNA sequences (AAT62511 and AAT13847) respectively code for
XX primatised forms (AAW01819 and AAW01820) of the light and heavy chains
XX of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
XX 7B6. Cloned 7B6 light and heavy variable genes are inserted into
XX an expression vector (pref. NEOSPLA) which contains human light and
XX heavy chain constant region genes to allow prodn. of primatised
XX antibody in e.g. CHO cells. Primatised 7C10 and 16C10 anti-B7.1
XX antibodies have also been produced (see also AAW01817-18 and AAW01821-
XX 22). The primatised antibodies inhibit the B7:CD28 pathway, making
XX them useful immunosuppressants for the treatment of autoimmune
XX disorders and graft-versus-host disease.
XX
SQ Sequence 720 BP; 178 A; 201 C; 192 G; 149 T; 0 other;

Query Match 99.8%; Score 718.4; DB 18; Length 720;
Best Local Similarity 99.9%; Pred. No. 7.2e-182;
Matches 719; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGCCTCCCTGCTCAGCTCTCCGCGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60
DB 1 ATGAGCCTCCCTGCTCAGCTCTCCGCGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60

QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACCTGGAGAGCGCGCTCC 120
DB 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACCTGGAGAGCGCGCTCC 120

QY 121 ATCTCTGTAGGCTTAGTCAAAAGCCTTAAACACAGTAATGGAGACACCTTCTGAGTTGG 180
DB 121 ATCTCTGTAGGCTTAGTCAAAAGCCTTAAACACAGTAATGGAGACACCTTCTGAGTTGG 180

QY 181 TATCAGCAGAGCCAGGCCAACCTCCAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240
DB 181 TATCAGCAGAGCCAGGCCAACCTCCAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240

QY 241 TCTGGGTCCCAACAGATTCAGCTCTCCACTGTCCCTTCCCATCACCTGGAGAGCGCGCTCC 300
DB 241 TCTGGGTCCCAACAGATTCAGCTCTCCACTGTCCCTTCCCATCACCTGGAGAGCGCGCTCC 300

QY 301 AGCGCAGTGGAGGCTGAGATGTTGGGGTTTATTCTCGGGCAAGGTACAAGGACTCCT 360
DB 301 AGCGCAGTGGAGGCTGAGATGTTGGGGTTTATTCTCGGGCAAGGTACAAGGACTCCT 360

QY 361 CCCACTTTCCGGCGAGGGACCAAGGTGGAATCAAACTGAGTGAAGTGAACGCCCTCCAA 420
DB 361 CCCACTTTCCGGCGAGGGACCAAGGTGGAATCAAACTGAGTGAAGTGAACGCCCTCCAA 420

Anderson DR, Brans P, Hanna N;
WPI; 1998-286601/25.
P-PSDB; AAW63762.

New monoclonal antibodies specific for B7.1 or B7.2 antigens and
inhibiting binding to CD28 - useful as specific immunosuppressants
for treating diseases that involve interactions between T and B
cells, e.g. Graft rejection or tumours

Example 7; Fig 4a; 87pp; English.

This sequence encodes a primate form of the antibody 786 light chain
from macaque. This sequence is used in a method which studies new
monoclonal antibodies (MAB's) that bind selectively to B7.1 (CD80) or to
B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
MAB's are specific immunosuppressants for treatment of diseases involving
T cell/B cell interactions, particularly autoimmune disease, specifically
idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
host diseases, B cell lymphoma, infections (including by human immune
deficiency virus) or inflammatory disease and tumours. Optionally the
MAB can be conjugated to a drug or toxin. MAB's, or their fragments, can
also be used as imaging agents and as vaccines or immunogens to develop
anti-idiotypic reagents. MAB's are optionally combined with other proteins
or small molecule immunosuppressants. Blocking B7/CD28 interactions
induces long-term, antigen-specific immunosuppression, i.e. it inhibits
production of interleukin-2 (IL-2), T cell proliferation and
antigen-specific immunoglobulin G (IgG) responses.

Sequence 720 BP; 178 A; 200 C; 193 G; 149 T; 0 other;

Query Match 100.0%; Score 720; DB 19; Length 720;
Best Local Similarity 100.0%; Pred. No. 2.7e-182;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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DB 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGGTGCTATTGCTCTCGTCCCGGGTCCAGTGGG 60

QY 61 GAAGTGTGTGATGACTCAGTCTCAGCTGTCCCTCCATCATCACCTGAGAGCCGGCTCC 120
DB 61 GAAGTGTGTGATGACTCAGTCTCAGCTGTCCCTCCATCATCACCTGAGAGCCGGCTCC 120

QY 121 ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGTAATGAGACACCTTCTGTAGTTGG 180
DB 121 ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGTAATGAGACACCTTCTGTAGTTGG 180

QY 181 TATCAGCAGAAGCCAGCCCAACCTCAAGGTCCTGATTTATAAGTTTCTAACCGGGAC 240
DB 181 TATCAGCAGAAGCCAGCCCAACCTCAAGGTCCTGATTTATAAGTTTCTAACCGGGAC 240

QY 241 TCTGGGGTCCACACAGATTTCAGCGCAGTGGGGCAGGCAGAGATTTCACACTGAAATC 300
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QY 301 AGCGCAGTGGAGCTCAAGATGTGGGGTTATTTCTCGGGCAGGTACAAGCACTCCT 360
DB 301 AGCGCAGTGGAGCTCAAGATGTGGGGTTATTTCTCGGGCAGGTACAAGCACTCCT 360

QY 361 CCCACTTTCGGCGGAGGACCAAGCTGGNAATCAAACTACAGTGGCTGGCACCACCTGTC 420
DB 361 CCCACTTTCGGCGGAGGACCAAGCTGGNAATCAAACTACAGTGGCTGGCACCACCTGTC 420

QY 421 TTCACTTCTCCCGGCATCTGATGAGCAGTTGAAATCTGGAACTGCTCTGTGTGTGCTG 480
DB 421 TTCACTTCTCCCGGCATCTGATGAGCAGTTGAAATCTGGAACTGCTCTGTGTGTGCTG 480

QY 481 CTGAATAACTTCTATCCCGAGAGGCGCAAGTACAGTGGAAAGGTGGATACAGCCCTCCAA 540
DB 481 CTGAATAACTTCTATCCCGAGAGGCGCAAGTACAGTGGAAAGGTGGATACAGCCCTCCAA 540

Qy	541	TCGGGTAACTCCAGGAGAGTGTGCACAGACGAGGACAGCAAGGACAGCACCTTACAGCCTC	600
Db	541	TCGGGTAACTCCAGGAGAGTGTGCACAGACGAGGACAGCAAGGACAGCACCTTACAGCCTC	600
Qy	601	AGCAGACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCTCCGAA	660
Db	601	AGCAGACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCTCCGAA	660
Qy	661	GTCAACCATCAGGGCCTGAGCTGCCCGTGCACAAAGAGCTTCAACAGGGGAGAGTGTGA	720
Db	661	GTCAACCATCAGGGCCTGAGCTGCCCGTGCACAAAGAGCTTCAACAGGGGAGAGTGTGA	720
RESULT 2			
ID	AAAS17244		
XX	AAAS17244	standard; DNA; 720 BP.	
AC	AAAS17244;		
XX			
DT	12-MAR-2002	(first entry)	
XX			
DE	DNA sequence of a primatised form of the light chain of 7B6 antibody.		
XX	Human; macaque monkey; light chain; primatised antibody; 7B6 antibody		
KW	neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist		
KW	B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;		
KW	tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;		
KW	graft-vs-host disease; immunosuppression; organ rejection;		
KW	interleukin-2; IL-2; mutant; ds.		
XX			
OS	Chimeric - Homo sapiens.		
OS	Chimeric - Macaca sp.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..720	
FT		/*tag= a	
FT		/product= "Light chain of 7B6 antibody"	
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PN	WO200109567-A1.		
XX			
PD	29-NOV-2001.		
XX			
PF	22-MAY-2001; 2001WO-US16364.		
XX			
PR	22-MAY-2000; 2000US-0576424.		
XX			
PA	(IDEC-) IDEC PHARM CORP.		
XX			
PI	Anderson DR, Hanna N, Brama P;		
XX			
DR	WPI; 2002-089895/12.		
DR	P-PSDB; AAU11540.		
XX			
PT	Use of monoclonal antibody which specifically binds to B7.1 antigen		
FT	CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,		
PT	treating cancer, graft-vs-host disease and autoimmune disease such as		
PT	allergy		
XX			
PS	Example 8; Fig 4a; 89pp; English.		
XX			
CC	The present invention relates to a new use of a monoclonal antibody		
CC	which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen		
CC	(CD86) for inducing the apoptosis of B7+ cells. The invention is		
CC	useful for treating diseases such as B cell cancer, lymphoma, a		
CC	cancer where B cells promote the growth and/or metastasis of tumours, a		
CC	B cell lymphoma, B cell leukaemia and autoimmune diseases such as		
CC	idiopathic thrombocytopenia purpura, systemic lupus, erythematous,		
CC	type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic		
CC	cancer, inflammatory bile disease, allergy, multiple sclerosis		
CC	or graft-vs-host disease. The antibody is useful for immunosuppression		
CC	in a human or animal and for treating or preventing resistance to or		
CC			

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 18:12:24 ; Search time 197.594 Seconds
(without alignments)
8205.894 Million cell updates/sec

Title: US-09-758-173-5

Perfect score: 720

Sequence: 1 ATGACCCCTCCCTGCTCAGCT.....TCACAGGGGAGAGTGTTGA 720

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	720	100.0	720	19	AAV35486
2	720	100.0	720	24	AAV35486
3	718.4	99.8	720	18	AAV62511
4	622	86.4	720	19	AAV61362
5	622	86.4	720	21	AAV78270
6	620.4	86.2	891	19	AAV66632
7	620.4	86.2	891	21	AAV78320
8	618.8	85.9	720	19	AAV61360
9	618.8	85.9	720	19	AAV61361

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11	618.8	85.9	720	21	AAA78269	Anti-human Fas imm
12	617.2	85.7	720	19	AAV61359	Anti-human Fas hum
13	617.2	85.7	720	21	AAA78267	Anti-human Fas imm
14	601.2	83.5	963	22	AAF44895	Human breast cance
15	599.4	83.2	720	21	AAA13924	Human PTHrP monocl
16	599.4	83.2	720	21	AAA13926	Human PTHrP monocl
17	598.8	83.2	720	21	AAA13927	Human PTHrP monocl
18	598.2	83.1	720	21	AAA13923	Human PTHrP monocl
19	596.6	82.9	720	21	AAA13920	Human PTHrP monocl
20	595.4	82.7	720	21	AAA13925	Human PTHrP monocl
21	593.4	82.4	720	21	AAA13922	Human PTHrP monocl
22	591.6	82.2	720	21	AAA13921	Human PTHrP monocl
23	587.8	81.6	720	21	AAA13928	Human PTHrP monocl
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25	582.2	80.9	772	20	AAZ24418	Human bladder tumo
26	561.2	77.9	726	17	AAI18060	Monoclonal antibod
27	558	77.5	720	21	ABK10999	DNA encoding prote
28	554.6	77.0	717	18	AAI26934	Murine anti-porcine
29	554.6	77.0	5300	18	AAI26938	3F4 human IgG4 exp
30	551.6	76.6	925	21	AAI27395	Human IGFAM-15 imm
31	549.2	76.3	740	22	AAI63373	Humanised 323/A3 (
32	549.2	76.3	740	22	AAI63377	Anti-Ep-CAM antibo
33	533	74.0	663	22	AAI20744	Human recombinant
34	527.6	73.3	737	13	AAQ25691	Sequence of the ch
35	520.6	72.3	799	24	AAI23241	Human lung specifi
36	519.2	72.1	727	21	AAI287965	Chimeric 6G4.2.5 a
37	519.2	72.1	729	16	AAI03380	Anti-IL-8 chimeric
38	519.2	72.1	729	18	AAV03226	Murine variable re
39	519.2	72.1	729	18	AAI93549	Chimeric monoclonal
40	519.2	72.1	729	18	AAI78594	Chimeric monoclonal
41	519.2	72.1	729	19	AAV44951	Anti-IL-8 mouse-hu
42	519.2	72.1	729	19	AAV10316	Chimeric Mab 6G4.2
43	519.2	72.1	729	19	AAV06417	Chimeric monoclonal
44	519.2	72.1	729	20	AAI90573	Chimeric 6G4.2.5 1
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ALIGNMENTS

RESULT 1
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ID AAV35486 standard; DNA; 720 BP.
XX
AC AAV35486;
XX
DT 29-SEP-1998 (first entry)
XX
DE Macaque primatized 7B6 light chain DNA.

XX Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW T cell/IB cell interaction; tumour; inflammation; imaging agent; vaccine;
KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
KW T cell proliferation; ss.
XX Macaca fascicularis.
OS

XX Key Location/Qualifiers
FH Key 1..720
FT CDS /*tag= a
FT /product= 7B6 light chain

XX WO9819706-A1.
XX
PD 14-MAY-1998.
XX
PF 29-OCT-1997; 97WO-US19906.
XX
PR 08-NOV-1996; 96US-0746361.
XX
PA (IDEC-) IDEC PHARM CORP.

Qy 718 TGA 720
Db 733 AGA 735

Search completed: April 6, 2003, 06:20:27
Job time : 1373.41 secs

Query Match 78.8%; Score 567.4; DB 12; Length 701;
 Best Local Similarity 91.5%; Pred. No. 2.1e-154; Mismatches 56; Indels 1; Gaps 1;
 Matches 612; Conservative 0; Mismatches 56; Indels 1; Gaps 1;

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 92 GATGTTGTGTGATCAGTCTCCACTCTCCCTGCGCGTCCACCTTTGAGAGCGGCTCC 151
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 152 ATCTCTGAGTCTAGTCAAGCCCTGCTGACACTGATGGAACACCTACTTGAATTGG 211
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 Db |||||
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 Db |||||

QY 481 CTGAATTAATCTTATCCAGAGGCGCAAGTACAGTGGAGGTGGAATCAACGCTGGA 540
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 VERSION BG740066
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 738)
 NIH-MGC <http://mgi.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
 Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM10628 row: n column: 09
 High quality sequence stop: 736.
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 BASE COUNT 187 a 204 c 188 g 159 t
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Query Match 78.6%; Score 565.8; DB 12; Length 738;
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 Matches 651; Conservative 0; Mismatches 67; Indels 5; Gaps 4;

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 Db |||||
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 Db |||||

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 Db |||||
 135 ATCTCTGAGTCTAGTGAAGCTCTCTACACAGTAATGGAACACCTATTTGAGTTGG 194
 Db |||||

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 Db |||||
 195 CTTCACAGAGCGGACCAAGCTCCAGGCTCTCTCAATATAAATTTCTAACCGGTT 254
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 Db |||||
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 Db |||||

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 Db |||||
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 Db |||||

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 Db |||||

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 Db |||||
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QY 600 CAGCAGCCTTCACTGAGCAAGCAGCACTACAGAAACACAAAGTCTACGCTCCGA 659
 Db |||||
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TITLE          NIH-MGC http://mgi.nci.nih.gov/
JOURNAL        National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT        Unpublished (1999)
                Contact: Robert Strausberg, Ph.D.
                Email: cgaabs@rmail.nih.gov
                Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
                cDNA Library Preparation: Ling Hong/Rubin Laboratory
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
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                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GCACACAG(G). Size-selected >500bp
                for average insert size 1.8kb. Library constructed by Ling
                Hong in the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH-MGC Library."
BASE COUNT     204 a 266 c 216 g 194 t
ORIGIN
Query Match    79.2%; Score 570.2; DB 12; Length 880;
Best Local Similarity 88.8%; Pred. No. 3.7e-155;
Matches 640; Conservative 0; Mismatches 78; Indels 3; Gaps 2;

Qy 1 ATGAGCTCCCTGCTCAGCTCCCTCGGGCTGCTATTGCTCTGCTCCCGGTCCAGTGGG 60
Db 11 ATGAGGCTCCCTGCTCAGCTCCCTCGGGCTGCTATTGCTCTGCTCCCGGTCCAGTGGG 70
Qy 61 GAAGTTGTGATGACTCAGTCTCAGTCTCCCTTCCCATCAGCTGGAGAGCGGCTCC 120
Db 71 GAAATTGTGATGACTCAGTCTCAGTCTCCCTTCCCATCAGCTGGAGAGCGGCTCC 130
Qy 121 ATCTCTGTAGTCTAGTCAAGACCTTAAACACAGTAAATGGAGACACCTTCTCAGTTGG 180
Db 131 ATCTCTGTAGTCTAGTCAAGACCTTCTGATACATGATGATACATCTTTCGATTTGG 190
Qy 181 TATCAGCAGAAGCCAGCCCAACCTCCCAAGGCTCTGATTTATATAGTTTCTTAACCGGGAC 240
Db 191 TACCTGCAGAAGCCAGCCCAAGGCTCTCCCAACCTCTGATTTATAGTTTCTTAACCGGGAC 250
Qy 241 TCTGGGGTCCAGACAGATTTCAGCGGCAGTGGGGGAGGAGGAGATTTTACACTGAATATC 300
Db 251 TCCGGGGTCCCTGACAGTTTCAGTGGCATGGATCAGGACAGATTTTACACTGAATATC 310
Qy 301 AGCGAGTGGAGCTGAAGATGTTGGGTTATTTCTCGGGCAAGGTACAGGACTCTCT 360
Db 311 AACAGATGGAGCTGACGATGTTGGGTTATTTACTGATGATGATGATGATGATGATGAT 370
Qy 361 CCACATTTCCGGCGGAGGACCAAGTGGAAATCAACGATCGGTGGTGGACCATCTGTC 420
Db 371 TTCACTTTCCGGCCCTGGGACCAAGTGGAAATCAACGATCGGTGGTGGACCATCTGTC 430

Qy 421 TTCACTTTCCGGCCCTGATGAGCAGTTGAAATCTGGAACCTGCTCTGTTGTGTGCTG 480
Db 431 TTCACTTTCCGGCCCTGATGAGCAGTTGAAATCTGGAACCTGCTCTGTTGTGTGCTG 490
Qy 481 CTGAATAACTTCTATCCAGAGAGGCCAAGTACAGTGGAGGTGGATTAACGCCCTCCAA 540
Db 491 CTGAATAACTTCTATCCAGAGAGGCCAAGTACAGTGGAGGTGGATTAACGCCCTCCAA 550
Qy 541 TCGGGTAACTCCCGAGGAGGTGTACAGAGCAGGACAGCAAGGACGACCTTACAGCTC 600
Db 551 TCGGGTAACTCCCGAGGAGGTGTGTACAGAGCAGGACAGCAAGGACGACCTTACAGCTC 610
Qy 601 AGCAGCA-CCCTGACGCTGAGCAAGCAGACGACGACGACGACGACGACGACGACG 659
Db 611 AGCAGCA-CCCTGACGCTGAGCAAGCAGACGACGACGACGACGACGACGACGACG 670
Qy 660 AGTCACCATCAGGGCTG--AGCTGCGCGCTGACCAAGAGCTTCAACAGGGGAGGTGT 717
Db 671 AGTCACCATCAGGGCTG--AGCTGCGCGCTGACCAAGAGCTTCAACAGGGGAGGTGT 730
Qy 718 T 718
Db 731 T 731

RESULT 14
LOCUS      BG547597
DEFINITION BG547597 701 bp mRNA Homo sapiens cDNA clone IMAGE:4703696 5',
            mRNA sequence.
ACCESSION  BG547597
VERSION     BG547597.1  GI:13546262
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            NIH-MGC http://mgi.nci.nih.gov/
            1 (bases 1 to 701)
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaabs@rmail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1542 row: i column: 09
            High quality sequence stop: 698.
            Location/Qualifiers
            1..701
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            /db_xref="taxon:9606"
            /clone="IMAGE:4703696"
            /lab_host="DH10B (T1 phage-resistant)"
            /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
            SfiI (ggccattggcc); Site 2: SfiI (ggccattggcc); 5' and
            3' adaptors were used in cloning as follows: 5' adaptor
            sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
            5'-ATTCTAGAGCGCGGCGGCGGACATG-dt(30)BN-3' (where B = A,
            C, or G and N = A, C, G, or T). Average insert size 1.9
            kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
            by PCR. This library was enriched for full-length clones
            and was constructed by Clontech Laboratories (Palo Alto,
            CA). Note: this is a NIH-MGC library."
BASE COUNT    169 a 199 c 185 g 148 t
ORIGIN

```


Db	68	GA	TAT	CGT	GAT	GACT	CA	GT	CT	CC	ACT	CT	CC	CT	CC	CGT	CA	CC	CT	CG	GAG	AG	CG	CG	CT	CC	127	
Qy	121	AT	CT	CT	G	T	A	G	T	CT	TA	AG	CA	AG	CT	T	A	A	A	C	A	C	A	G	A	C	CT	180
Db	128	AT	CT	CT	G	C	A	G	T	CT	TA	AG	CA	AG	CT	CT	C	G	C	A	T	A	T	A	T	A	G	187
Qy	181	T	A	T	C	A	C	A	G	C	C	A	A	C	T	C	C	A	A	G	G	T	T	T	A	A	G	240
Db	188	T	A	C	T	C	A	A	G	C	C	A	A	G	C	A	G	C	T	C	T	G	T	T	T	T	T	247
Qy	241	T	C	T	G	G	G	T	C	C	A	G	A	T	T	C	A	G	G	G	G	C	A	G	A	T	T	300
Db	248	T	C	G	G	G	T	C	C	T	G	A	G	T	T	C	A	G	G	C	A	G	A	T	T	T	T	307
Qy	301	A	G	C	A	G	T	G	G	A	G	T	T	T	T	T	C	T	G	G	G	A	A	G	T	T	T	359
Db	308	A	G	C	A	G	T	G	G	A	G	T	T	T	T	T	A	T	A	T	G	C	A	T	T	T	T	367
Qy	360	T	C	C	A	C	T	T	T	C	G	G	C	A	G	G	A	C	A	A	G	T	G	A	A	T	C	419
Db	368	A	T	G	T	A	C	A	C	T	T	T	T	T	T	T	C	A	A	G	T	G	G	A	T	T	T	427
Qy	420	C	T	T	C	A	T	T	T	C	C	G	C	C	A	T	C	T	G	A	A	T	C	T	G	T	T	479
Db	428	C	T	T	C	A	T	T	T	C	C	G	C	C	A	T	C	T	G	A	A	T	C	T	G	T	T	487
Qy	480	G	C	T	G	A	T	A	A	C	T	T	A	T	C	C	A	G	A	G	G	C	C	A	A	G	T	539
Db	488	G	C	T	G	A	T	A	A	C	T	T	A	T	C	C	A	G	A	G	G	C	C	A	A	G	T	547
Qy	540	A	T	C	G	G	T	A	A	C	T	C	C	A	G	A	G	T	G	T	C	A	G	A	G	A	G	599
Db	548	A	T	C	G	G	T	A	A	C	T	C	C	A	G	A	G	T	G	T	C	A	G	A	G	A	G	607
Qy	600	C	A	G	C	A	C	C	T	T	G	A	A	G	C	A	C	T	A	C	G	A	A	A	C	A	A	659
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Qy	660	A	G	T	C	C	C	A	T	C	A	G	G	C	T	G	A	C	T	C	G	C	C	T	C	A	A	718
Db	668	A	G	T	C	C	C	A	T	C	A	G	G	C	T	G	A	C	T	C	G	C	C	T	C	A	A	726

RESULT 12
BQ709417
LOCUS BQ709417 958 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_7976027 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214761
5', mRNA sequence.

SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE	1 (bases 1 to 958)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

FEATURES	SOURCE
1. Geographical Location: The study area is located in the northern part of the state, covering a total area of 1,200 square kilometers.	State Geographical Information System (GIS) data.
2. Population Density: The population density is relatively low, with an average of 150 people per square kilometer.	Census Bureau data.
3. Climate: The climate is semi-arid, with annual rainfall ranging from 400 to 600 millimeters.	Local meteorological station records.
4. Topography: The terrain is mostly flat, with some low hills and valleys.	Aerial photography and topographic maps.
5. Vegetation: The vegetation is primarily dry grassland and shrubs.	Field observations and satellite imagery.
6. Water Resources: There are several small rivers and streams in the area.	Hydrological survey data.
7. Soil Types: The soil is mostly sandy and loamy.	Soil sampling and analysis.
8. Land Use: The land is primarily used for agriculture and grazing.	Land use maps and surveys.
9. Infrastructure: There is a network of roads and a few small towns.	Infrastructure maps and reports.
10. Environmental Issues: The main environmental issues are drought and soil erosion.	Environmental impact assessments.

Plate: LLCM2382 row: j column: 10
High quality sequence stop: 574.

BG755003
 LOCUS BG755003 880 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602711509F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851723 5',
 mRNA sequence.

REFERENCE
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1622 row: b column: 18
 High quality sequence stop: 725.

FEATURES
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 1. .908
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 /db_xref="taxon:9606"
 /clone="IMAGE:4764593"
 /clone_lib="NIH_MGC_48"
 /tissue_type="Primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."
 BASE COUNT 219 a 250 c 238 g 201 t
 ORIGIN

Query Match 80.3%; Score 578.4; DB 12; Length 908;
 Best Local Similarity 90.4%; Pred. No. 1.9e-157;
 Matches 651; Conservative 0; Mismatches 66; Indels 3; Gaps 3;
 QY 1 ATGAGCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGGTCCCGGGTCCAGTGGG 60
 DB 8 ATGAGGCTCCCTGCTCAGCTCCTCGGGCTGCTAATGCTCTGGGCTCTCTGGATCCAGTGGG 67
 QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCTCCCTCCCATCACACCTGAGAGCGCGCCCTCC 120
 DB 68 G-ATATGTGATGACTCAGTCTCCACTGTCTCCCTGCCGTGAGAGCGCGCCCTCC 126
 QY 121 ATCTCTGTAGTCTTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCTCTGAGTTGG 180
 DB 127 ATCTCTGCAAGTCTAGTCAGAGCCTCTGATAGTAAATGGATACAACTATTGGATTGG 186
 QY 181 TATCAGCAGAGCCAGGCCAACCCTCAAGCTCTGATTTAAGTTTCTAACCGGGAC 240
 DB 187 TACTCTGAGAAGCCAGG-CAGTCTCCACAGCTCTGATCTATTGGGTTCTAATCGGGCC 245
 QY 241 TCTGGGGTCCACAGAGATTACCGGCAGTGGGGCAGGACAGATTTCACACTGAAATTC 300
 DB 246 TCGGGGTCCCTCAGAGTTCACTGGCAGTGGATCAGGCACAGATTTCACACTGAAATTC 305
 QY 301 AGCGCAGTGAGGCTGAAGATGTGGGGTTTATTCTCGGGCAAGGTACAAGGACTCTCT 360
 DB 306 AGCAGAGTGAGGCTGAGGATGTGGGGTTTATTCTGTCATGCAAGCTCTACAAATTCG 365
 QY 361 CCACATTCGGCGGAGGACCAAGTTGGAATCAACAGTACGGTGGCTGCACATCTGTC 420
 DB 366 CTCACATTCGGCGGAGGACCAAGTTGGAATCAACAGTACGGTGGCTGCACATCTGTC 425
 QY 421 TTCACTCTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGSCCTG 480
 DB 426 TTCACTCTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGSCCTG 485
 QY 481 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAA 540

Db 486 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAAGCCCTCAA 545
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 DB 546 TCGGGTAATCCCGAGGAGAGTGTTCACAGAGCAGCAGCAGCAGCAGCAGCAGCAGCCTC 605
 QY 601 AGCAGCAGCCTGAGCCTGAGCAAGAGAGACTACAGAGAAACACAAAGTCTACGCTCGAA 660
 DB 606 AGCAGCAGCCTGAGCCTGAGCAAGAGAGACTACAGAGAAACACAAAGTCTACGCTCGAA 665
 QY 661 GTCAACCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGAGAGTGTGTA 720
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RESULT 11
 BG758795 859 bp mRNA linear EST 15-MAY-2001
 LOCUS 60271315F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853557 5',
 DEFINITION mRNA sequence.
 ACCESSION BG758795
 VERSION BG758795.1 GI:14069448
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 859)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1699 row: m column: 14
 High quality sequence stop: 724.

FEATURES
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 1. .859
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 /clone="IMAGE:4853557"
 /clone_lib="NIH_MGC_48"
 /tissue_type="Primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."
 BASE COUNT 201 a 251 c 215 g 191 t 1 others
 ORIGIN

Query Match 80.3%; Score 578; DB 12; Length 859;
 Best Local Similarity 88.6%; Pred. No. 1.9e-157;
 Matches 637; Conservative 0; Mismatches 81; Indels 1; Gaps 1;
 QY 1 ATGAGCTCCCTGCTCAGCTCCTCGGGCTCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60
 DB 8 ATGAGGCTCCCTGCTCAGCTCCTCGGGCTCTAATGCTCTGGGCTCTTGGATCCAGTGGG 67
 QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCTCCCTCCCATCACACTGAGAGCGCGCCCTCC 120

Db 182 CAGGCCAGTCTCCACAGCTCCTGATCTATGAAGTTTCCACCGGTCTCTGGAGTGCCA 241

Qy 253 GACAGATTTCACGCGCAGTGGGGCAGGACAGATTTACACTGAAAAATCAGCGCAGTGGAG 312

Db 242 GATAGGTTTCAGTGGCAGCGGTTCAGGACAGATTTACACTGAAAAATCAGCGGTGGAG 301

Qy 313 GCTGAAGATTGGGGTTTATTTCTGGGGCAAGGTACAAAGACTCTCCACTTTCGGC 372

Db 302 GCTGAGGATGTTGGGGTTTATTACTGATGCAAAAGTATACAGCTTCTCTCACTTTCGGC 361

Qy 373 GGAGGACCAAGGTGGAATCAAAAGTACGAGTGGCTGCACCTCTCTTCACTTTCGGC 432

Db 362 GGAGGACCAAGGTGAGATCAAAAGTACGAGTGGCTGCACCTCTCTTCACTTTCGGC 421

Qy 433 CCATCTGATGAGCAGTGTGAATCTGGAACCTGCCTCTGTTGTGTCCTGCTGAATTAATTC 492

Db 422 CCATCTGATGAGCAGTGTGAATCTGGAACCTGCCTCTGTTGTGTCCTGCTGAATTAATTC 481

Qy 493 TATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATTAAGCCCTCCAAATCGGGTAATCTCC 552

Db 482 TATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATTAAGCCCTCCAAATCGGGTAATCTCC 541

Qy 553 CAGGAGAGTCTCAGAGCAGGACAGCAGGACAGCAGCTTACAGCCTCAGCAGCACCCTG 612

Db 542 CAGGAGAGTCTCAGAGCAGGACAGCAGGACAGCAGCTTACAGCCTCAGCAGCACCCTG 601

Qy 613 ACGTGAGCAAGAGCAGACTACGAGAAACACAAAGTCTAGCCCTGCGAAGTCAACCCATCAG 672

Db 602 ACGTGAGCAAGAGCAGACTACGAGAAACACAAAGTCTAGCCCTGCGAAGTCAACCCATCAG 661

Qy 673 GGCTGAGCTGCGCCGTCAAAAGAGCTTCAACAGGGGAGGTGTT 718

Db 662 GGCTGAGCTGCGCCGTCAAAAGAGCTTCAACAGGGGAGGTGTT 707

RESULT 9

BI768966 720 bp mRNA linear EST 25-SEP-2001

LOCUS 60358111F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5207427 5',

DEFINITION mRNA sequence.

ACCESSION BI768966

VERSION BI768966.1 GI:15760544

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 720) NIH-MGC http://mgi.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaabs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L14M11520 row: f column: 04 High quality sequence stop: 719. Location/Qualifiers 1..720 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5207427" /clone_lib="NIH_MGC_122" /lab_host="DH108" /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT

primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH MGC Library."

BASE COUNT 175 a 204 c 185 g 156 t

ORIGIN

Query Match 81.6%; Score 587.2; DB 13; Length 720;

Best Local Similarity 92.1%; Pred. No. 3.5e-160;

Matches 641; Conservative 0; Mismatches 53; Indels 2; Gaps 2;

Qy 1 ATGAGCCTCCCTGCTCAGCTCTCGGGC-TGCTATTGCTCTGCGTCCCGGGTCCAGTGG 59

Db 26 ATGAGCCTCCCTGCTCAGCTCTCGGGCTTGTAAATGCTCTGGGTCCAGGATCCAGTGG 85

Qy 60 GGAAGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACACTCGAGAGCGGGCTC 119

Db 86 GGATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTTGGACAGCGGGCTC 145

Qy 120 CATCTCTGTAGGTCTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCTCTGAGTTG 179

Db 146 CATCTCTGCAAGTCTAGTCAAAGCCTCGTATACAGTATGGAACACCTACTTGAATTG 205

Qy 180 GTATCAGCAGAAGCAGCGCCAACTCCAGGCTCTGATTTATAGGTTTCTAACCCGGGA 239

Db 206 GTTTTCAGCAGAGGCGAGCCCAATCTCCAAGCGCTTAATTTATAGGTTTCTAACCCGGGA 265

Qy 240 CTCTGGGTCCTCAGACAGATTTCAGCGCAGTGGGGCAGGACAGATTTTCACACTGAAAAT 299

Db 266 CTCTGGGTCCTCAGACAGATTTCAGCGCAGTGGGTGAGGCTGATTTTCACACTGAAAAT 325

Qy 300 CAGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGCGGGCAAGGTACAAGGACTCC 359

Db 326 CAGCAGGTCGAGGCTGAGGATGTTGGGGTTTATTTACTGTCATGCAAGGTACACACTGGCC 385

Qy 360 TCCCACTTTCCGGCGGAGGACCAAGGTGGAAATCAAAGTACGGTGGCTGCACCATCTGT 419

Db 386 GTACACTTTTGGC-CAGGGACCAAGCTGGAGATCAAAAGTCAAACTGTGGCTGCACCATCTGT 444

Qy 420 CTTCACTTTCCCGCCATCTGATGAGCAGTTTGAATCTGGAACCTGCTCTGTTGTGGCT 479

Db 445 CTTCACTTTCCCGCCATCTGATGAGCAGTTTGAATCTGGAACCTGCTCTGTTGTGGCT 504

Qy 480 GCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATTAACGCCCTCCA 539

Db 505 GCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATTAACGCCCTCCA 564

Qy 540 ATCGGGTAACCTCCAGGAGAGTGTCAACAGCAGGACAGCAGGACAGCAGCCTACAGCCT 599

Db 565 ATCGGGTAACCTCCAGGAGAGTGTCAACAGCAGGACAGCAGGACAGCAGCCTACAGCCT 624

Qy 600 CAGCAGCAGCCTGAGCGTGGCAAGGACAGCTACGAGAAACACAAAGTCTACGCTCGGA 659

Db 625 CAGCAGCAGCCTGAGCGTGGCAAGGACAGCTACGAGAAACACAAAGTCTACGCTCGGA 684

Qy 660 AGTCAACCCATCAGGCGCTGAGCTCGCCGTCACAAA 695

Db 685 AGTCAACCCATCAGGCGCTGAGCTCGCCGTCACAAA 720

RESULT 10

BI7685179 908 bp mRNA linear EST 01-MAY-2001

LOCUS 602637065F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4764593 5',

DEFINITION mRNA sequence.

ACCESSION BI7685179

VERSION BI7685179.1 GI:13916576

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2464 row: j column: 02
High quality sequence stop: 645.
Location/Qualifiers
1. .952
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6277729"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: "Homo sapiens"; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 242 a 273 c 252 g 227 t 1 others
ORIGIN
Query Match 82.2%; Score 591.8; DB 14; Length 995;
Best Local Similarity 89.3%; Pred. No. 2e-161;
Matches 634; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1 ATGAGGCTCCCTGCTCAGCTCCCTGGGCTGCTATGCTCTGGTCCCGGNCAGTGGG 60
DB 7 ATGAGGCTCCCTGCTCAGCTCCCTGGGCTGCTAAATGCTCTGGGTCTCTGGATCCAGTGGG 66
QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACACTGGAGAGCGGCTCC 120
DB 67 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTGTCACCCCTGGAGAGCGGCTCC 126
QY 121 ATCTCTGTAGTCTAGTGAAGCCTTAAACACAGTAATGAGACACCTTCTCTGATGG 180
DB 127 ATCTCTGTGAGTCTAGTGAAGCCTTCTGATAGTAAATGAGTAACTATTTAGATTGG 186
QY 181 TATCAGCAGAGCCAGGCAACTCCAGGCTCTCATTTATAAGTTTCTAACGGGAC 240
DB 187 TACTCTGAGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGGGTCTTAATCGGGCC 246
QY 241 TCTGGGGTCCACAGAGATTTCAGCGGAGTGGGGCAGGAGACAGATTTCACACTGAAATC 300
DB 247 TCGGGGTCTCTACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 306
QY 301 AGCGAGTGGAGGCTGAAGATTTGGGGTTTATTTCTGGGGCAAGGTACAAGACTCTCT 360
DB 307 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTTACTGATGCAAGCTCTACAAATCCG 366
QY 361 CCCACTTTCGGCGGAGGACCAAGTGGAAATCAACAGTACCGTGGCTGCACCATCTGTC 420
DB 367 TACACTTTTGGCCAGGGGACCAAGCTGGAGATCAACAGCAACTGTGGCTGCACCATCTGC 426
QY 421 TTCATCTTCCCGGCATCTGATGAGCAGTTGAAATCTGGAACCTCCCTCTGTGTGTCCTG 480
DB 427 TTCATCTTCCCGGCATCTGATGAGCAGTTGAAATCTGGAACCTCCCTCTGTGTGTCCTG 486
QY 481 CTGAATAACTTTCTATCCAGAGAGGCAAGTAACAGTGGAGTGGATACAGCCCTCCAA 540
DB 487 CTGAATAACTTTCTATCCAGAGAGGCAAGTAACAGTGGAGTGGATACAGCCCTCCAA 546
QY 541 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACGACCTTACAGCCTC 600
DB 547 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACGACCTTACAGCCTC 606
QY 601 AGCAGCACTCTGAGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGGAA 660

Db 607 AGCAGCACCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGGAA 666
QY 661 GTACCCATCAGGCGCTGAGCTCGCCGCTCAGAAAGAGCTTCAACAGGG 710
DB 667 GTACCCATCAGGCGCTGAGCTCGCCGCTCAGAAAGAGCTTCAACAGGG 716
RESULT 8
LOCUS BG758592 952 bp mRNA linear EST 15-MAY-2001
DEFINITION 602712820F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853045 5', mRNA sequence.
ACCESSION BG758592
VERSION BG758592.1 GI:14069245
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 952)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1698 row: h column: 06
High quality sequence stop: 857.
Location/Qualifiers
1. .952
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/db_xref="taxon:9606"
/clone="IMAGE:4853045"
/clone_lib="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 233 a 284 c 240 g 215 t
ORIGIN
Query Match 82.1%; Score 590.8; DB 12; Length 952;
Best Local Similarity 89.8%; Pred. No. 3.7e-161;
Matches 634; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 13 GCTCAGTCTCTCGGGCTGCTATTTGCTCTGGTCTCCCGGTCAGTGGGAGTTGTGATG 72
DB 2 GCTCAGTCTCTCGGGCTGCTAAATGCTCTGGATACCTGGATCCAGTGCAGATATTGTGATG 61
QY 73 ACTCAGTCTCCACTGTCCCTTCCCATCACACTGGAGCGGCTCCATCTCTGTGAGG 132
DB 62 ACCCAGACTCTCCTCTCTGTCTGGTCCACCTTGGACAGCGGCTCCATCTCTCTCAAG 121
QY 133 TCTAGTCAAGACCTTAAACACAGTAATGGAGACACCTTCTCTGAGTTGGTATCAGCAGAAG 192
DB 122 TCTAGTCAGACCTCTCTGTCATAGTGAAGACCTATTGTGATTGGTACCTCAGCAGAAG 181
QY 193 CCAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTTAACCGGGACTCTTGGGGTCCCA 252

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Db 241 TGGAGTCCAGATAGTTCACTGGCAGCGGTCAGGACAGATTTTCACTGAAATCAG 300
Qy 303 CGCAGTGAGGCTGAAGATGTTGGGGTTTATTTCTGGCGGCAAGGTACAAGGACTCCTCC 362
Db 301 CCGGGTGAGGCTGAGGATGTTGGGGTTTATTTCTGCATGCAAGATATACAGTTTCTCTCT 360
Qy 363 CACTTTCGGCGGAGGACCAAGGTGGAAATCAAAAGCTACGGTGCGTGCACCAATCTGCTT 422
Db 361 CACTTTCGGCGGAGGAGCAAGGTGGAGATCAAAACGAATGTGGCTGCACCAATCTGCTT 420
Qy 423 CATCTTCCCGGCATCTGATGAGCAGTTGAAATCTGGAACCTGGAACCTCTGTGTGCTGCT 482
Db 421 CATCTTCCCGGCATCTGATGAGCAGTTGAAATCTGGAACCTGCTGTGTGCTGCTGCT 480
Qy 483 GAATAAATCTTATCCAGAGAGGCAAGTACAGTGGAAAGTGGATTAACGCCCTCCAATC 542
Db 481 GAATAAATCTTATCCAGAGAGGCAAGTACAGTGGAAAGTGGATTAACGCCCTCCAATC 540
Qy 543 GGGTAATCTCCAGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACTTACAGCTTCAG 602
Db 541 GGGTAATCTCCAGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACTTACAGCTTCAG 600
Qy 603 CAGCACTCTGAGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGT 662
Db 601 CAGCACTCTGAGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGT 660
Qy 663 CACCATCAGGGCTGAGCTGCGCCGTCACAAAGAGCTTCAACAGGGG 710
Db 661 CACCATCAGGGCTGAGCTGCGCCGTCACAAAGAGCTTCAACAGGGG 708

RESULT 6
BM007723
LOCUS 603617168F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440961 5',
DEFINITION mRNA sequence.
ACCESSION BM007723
VERSION 1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabbs-f@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1914 row: h column: 18
High quality sequence stop: 724.
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1..726
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/clone="IMAGE:5440961"
/clone_lib="NIH MGC 113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
SuperScript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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```
BASE COUNT 181 a 200 c 193 g 152 t
ORIGIN
Query Match 82.3%; Score 592.4; DB 13; Length 726;
Best Local Similarity 90.8%; Pred. No. 1.1e-161;
Matches 654; Conservative 0; Mismatches 61; Indels 5; Gaps 2;
Qy 1 ATGAGCTCCCTCGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60
Db 8 ATGAGCTCCCTCGCTCAGCTCCTCGGGCTGCTATTGCTCTGGTCCCAAGATCCAGTGGG 67
Qy 61 GAAGTTGATGACTCAGTCTCCTGCTCCCTTCCCATCACACTGGAGAGCGCGCTCC 120
Db 68 GATGTTGATGACTCAGTCTCCTGCTCCCTTCCCTGCGCTCACCTTTGGACAGCGCGCTCC 127
Qy 121 ATCTCTCTGAGTCTAGTCAAAAGCCTTAAACACAGTAATGAGACACCTTCTCTGAGTTGG 180
Db 128 ATCTCTCTGAGTCTAGTCAAAAGCCTTCTGATACAGTATGAAACACCTTCTCTGAGTTGG 187
Qy 181 TATCAGCAGAACCCAGGCGCAACCTCCAAGGCTCTCTGATTTATAAGGTTTCTAACCGGAC 240
Db 188 TTTTACAGCAGAGCCAGGCGCAATCTCCAAGGCGCTAATTTATAAGGTTTCTAACCGGAC 247
Qy 241 TCTGGGTCCCAAGACAGATTTACGGGAGTGGGGAGGAGAGATTTCACTGAAAAATC 300
Db 248 TCTGGGTCCCAAGACAGATTTACGGGAGTGGGGAGGAGAGATTTCACTGAAAAATC 307
Qy 301 AGCGCAGTGGAGGCTGAAGATGTTGGGGTATTATTTCTCGGGGCAAGGTACAAGGACTCCT 360
Db 308 AGCAGGTTGGAGGCTGAGATGTTGGGGTATTATTTCTGATGCAAGGTACACACTGGGCGG 367
Qy 361 CCCACTTTCCGCGAGGAGGACCAAG---GTGGAATCAAAAGTACGGTGGCTGCACCATC 416
Db 368 ATCACTTTCCGCGAGGACCAAGAGATGTGGAGATTAAACGAACTGTGGCTGCACCATC 427
Qy 417 TGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCTCTGTTGTGTG 476
Db 428 TGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCTCTGTTGTGTG 487
Qy 477 CCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCT 536
Db 488 CCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCT 547
Qy 537 CCAATCGGGTAACTCCCAAGGAGAGTGTACAGAGCAGACAGCAAGGACAGCAGCTACAG 596
Db 548 CCAATCGGGTAACTCCCAAGGAGAGTGTACAGAGCAGACAGCAGCAGCAGCAGCTACAG 607
Qy 597 CCTCAGCAGACCTTGACGCTGAGCAAGAGAGACTACGAGAAACACAAAAGTCTACGCCCTG 656
Db 608 CCTCAGCAGACCTTGACGCTGAGCAAGAGAGACTACGAGAAACACAAAAGTCTACGCCCTG 667
Qy 657 CGAAGTCAACCATCAGGGCCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGAGAGTG 716
Db 668 CGAAGTCAACCATCAGGGCCTGAGCTCG-CCGTCAAAAAGAGCTTCAACAGGGAGAGTG 726

RESULT 7
BM012430
LOCUS BM012430
DEFINITION AGENCOURT_8352203 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277729
5', mRNA sequence.
ACCESSION BM012430
VERSION BM012430.1 GI:21851329
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
```

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10611 row: k column: 01
High quality sequence stop: 866.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4752888"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 226 a 262 c 219 g 211 t

ORIGIN

Query Match 82.9%; Score 597.2; DB 12; Length 918;
Best Local Similarity 91.0%; Pred. No. 4.9e-163;
Matches 646; Conservative 0; Mismatches 63; Indels 1; Gaps 1;
QY 9 CCTGTCTCAGCTCCTCGGGCTGCTATTGCTCTCGCTCCCGGGTCCAGTGGGGAAGTGT 68
DB 1 CCTGTCTCAGCTCCTCGGGCTGCTATTGCTCTGGTCCAGCATCCAGTGGGGAAGTGA 60
QY 69 GATGACTCAGTCTCCACTGTCCTCCATCAACCTGAGAGCGGCTCCATCTCCTG 128
DB 61 GATGACTCAGTCTCCACTCTCCCTGCGCTCACCTTGGACAGCGGCTCCATCTCCTG 120
QY 129 TAGGTCTAGTCAAGGCTTAACACAGTAGTAAGAGACACTTCTCAGTGGTATCAGCA 188
DB 121 TAGGTCTAGTCAAGGCTCGTCTATAGTAAGTAAGTAACCTACTTGAATTTGTTTCAGCA 180
QY 189 GAAGCCAGGCAACCTCCAGGCTCTGATTTTATAGGTTTCTAACCGGACTCTGGGGT 248
DB 181 GAGCCAGGCCATCTCCAGGGCGCTAATTTATCAGTTTCTATCGGAGTCTGGGGT 240
QY 249 CCAGACAGATTGAGCGGAGTGGGCGAGGACAGATTTTACACTGAAAATCAGCGCAGT 308
DB 241 CTCAGACAGATTGAGCGGCGAGCGGTCAGGCACTGATTTTACACTGAAAATCAGCAGGT 300
QY 309 GGAGGCTGAGATGTTGGGGTTTATTTCTCGGGCAAGGTACAGGACTCCTCCCACTTT 368
DB 301 GGAGGCTGAGATGTTGGGGTTTATTTACTGCATGCAAGGAACACACTGGCCTCACACTTT 360
QY 369 CGGCGGAGGACCAAGGTGGAATCAAACTGAGGTGGGTGACCACTCTGTCTTATCTT 428
DB 361 TGSC-CAGGACCAAGTTGGAGATCAACCGAATCTGGCTGCACCACTCTGTCTTATCTT 419
QY 429 CCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTGCTGCTGAATAA 488
DB 420 CCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTGCTGCTGAATAA 479
QY 489 CTTCTATCCAGAGGCCAAAGTACNGTGGAGGTGGATTAAGCCCTCAATCCGGTAA 548
DB 480 CTTCTATCCAGAGGCCAAAGTACAGTGGAAAGTGGATTAAGCCCTCAATCCGGTAA 539
QY 549 CTCAGGAGGTGTACAGAGCAGGACCAAGGACAGCACTACAGCTCAGCAGCAC 608
DB 540 CTCAGGAGAGTGTACAGAGCAGGACCAAGGACAGCACTACAGCTCAGCAGCAC 599
QY 609 CTTGACGCTGAGCAAGCAGACTACGAGAAACACAAGTCTACGCTGCGAAGTCAACCA 668
DB 600 CTTGACGCTGAGCAAGCAGACTACGAGAAACACAAGTCTACGCTGCGAAGTCAACCA 659

QY 669 TCAGGGCCTGAGCTCGCCGCTCACAAGAGCTTCAACAGGGAGAGCTTT 718
DB 660 TCAGGGCCTGAGCTCGCCGCTCACAAGAGCTTCAACAGGGAGAGCTTT 709
RESULT 5
LOCUS BQ708918 898 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8495209 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301714
5', mRNA sequence.
ACCESSION BQ708918
VERSION BQ708918.1 GI:21847817
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 898)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2518 row: a column: 11
High quality sequence stop: 664.
Location/Qualifiers
1. .898
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/note="Organ: spleen; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 202 a 264 c 228 g 203 t 1 others
ORIGIN
Query Match 82.6%; Score 594.4; DB 14; Length 898;
Best Local Similarity 90.0%; Pred. No. 3.2e-162;
Matches 637; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
QY 3 GAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGGA 62
DB 1 GGGGCTCCCTGCTCAGCTCCTCGGGCTGCTAATGCTCTGGATCCTGGATCCAGTGGAGA 60
QY 63 AGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACACCTGGAGAGCGGCTCCAT 122
DB 61 TATTGTGATGACCCAGACTCCACTCTCTGTGCGTCACCCCTGGACAGCGGCTCCAT 120
QY 123 CTCCTGTAGTCTAGTCAAGCCTTAAACACAGTAATGGAGACACCTTCTGTAGTTGGTA 182
DB 121 CTCCTGCAAGTCTAGTCAGAGCCTCTCCATAGTAGTGAAGAACCTTTTGTATTGGTA 180
QY 183 TCACAGAGCCAGCCCAACCTCCAGGCTCTGATTTTATAAGGTTTCTAACCGGACTC 242
DB 181 CTTGAGAAAGCCAGGCGAGCCTCCACAGCTCCTGATCTATGAGGTTTCCAAACCGGTTCTC 240
QY 243 TGGGTCCTCCAGACAGATTGAGCGGCTGAGGCGGAGGACAGATTTCACACTGAAATCAG 302


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source
1. 816
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5183446"
/lab_host="NIH_MGC_116"
/lab_host="DH10B"
/notes="Organ: pooled colon, kidney, stomach; Vector:
PCMV-SPORE6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dt primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH MGC library."
BASE COUNT 194 a 238 c 208 g 176 t
ORIGIN

Query Match 85.9%; Score 618.8; DB 13; Length 816;
Best Local Similarity 91.4%; Pred. No. 2.3e-169;
Matches 656; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 1 ATGAGGCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGGTCCCGGGTCCAGTGGG 60
|
Db 10 ATGAGGCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGGTCCCGGGTCCAGTGGG 69
|
Qy 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCTTCCCATCACACCTGGAGAGCGGCTCC 120
|
Db 70 GATGTTGTGATGACTCAGTCTCCACTGTCCTTCCCATCACACCTGGAGAGCGGCTCC 129
|
Qy 121 ATCTCTGTAGTCTAGTCAAGCCTTAACACAGTAAATGAGACACCTTCTGTGATGG 180
|
Db 130 ATCTCTGTAGTCTAGTCAAGCCTTCTGATGATGATGATGATGATGATGATGATG 189
|
Qy 181 TATCAGCAGAGCGGCAACCTCCAGGCTCCTGATTTATAGGTTTCTAACCGGAC 240
|
Db 190 TTTACAGAGGCGGCGGCAATCTCCAGGCGCTTAATTTATAGGTTTCTAACCGGAC 249
|
Qy 241 TCTGGGTTCCAGACAGATTCAGCGGCACTGGGGCAGGACAGATTTTCACTGAAATC 300
|
Db 250 TCTGAGGTTCCAGACAGATTCAGCGGCACTGGGGCAGGACAGATTTTCACTGAAATC 309
|
Qy 301 AGCGCAGTGGAGCTCAAGATGTTGGGTTTATTTCTCGGCGCAAGTACAGGACTCT 360
|
Db 310 AGCAGGTTGGAGCTGAGGATGTTGGGTTTATTTCTGATGCAAGGATACCTCTCGG 369
|
Qy 361 CCCACTTTCCGGCGGAGGACCAAGGTGGAATCAAACTGACGTGGCTGCACCATCTGTC 420
|
Db 370 CGGACGTTCCGCCAAGGACCAAGGTGGAATCAAACTGACGTGGCTGCACCATCTGTC 429
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Qy 421 TTCACTTTCCCGCATCTGATAGCAGTTGAAATCTGGAATCTGCCTCTGTTGTGCTTG 480
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Db 430 TTCACTTTCCCGCATCTGATAGCAGTTGAAATCTGGAATCTGCCTCTGTTGTGCTTG 489
|
Qy 481 CTGAATTAATCTTATCCAGAGGCGCAAGTACAGTGGAGTGAATACCGCTCCAA 540
|
Db 490 CTGAATTAATCTTATCCAGAGGCGCAAGTACAGTGGAGTGAATACCGCTCCAA 549
|
Qy 541 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGCAGCAGCTACAGCTTC 600
|
Db 550 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGCAGCAGCTACAGCTTC 609
|
Qy 601 AGCAGCAGCTGAGCTGAGCAAGGAGACTACGAGAAACACAAAGTCTACGCTCGGAA 660
|
Db 610 AGCAGCAGCTGAGCTGAGCAAGGAGACTACGAGAAACACAAAGTCTACGCTCGGAA 669
|
Qy 661 GTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAGGCTTCAACAGGGGAGAGTGT 718
|
Db 670 CTCACCATCAGGCGCTGAGCTCGCCGTCACAAAGGCTTCAACAGGGGAGAGTGT 727
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RESULT 2
BM007808
LOCUS
DEFINITION
603617276F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440962 5',
mRNA sequence.
BM007808
VERSION
BM007808.1 GI:16522162
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 774)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1914 row: h column: 19
High quality sequence stop: 770.
FEATURES
Location/Qualifiers
1..774
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/clone="IMAGE:5440962"
/lab_host="NIH_MGC_113"
/notes="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 187 a 224 c 203 g 160 t
ORIGIN

Query Match 84.8%; Score 610.6; DB 13; Length 774;
Best Local Similarity 91.8%; Pred. No. 5.4e-167;
Matches 657; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

Qy 1 ATGAGCTCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGG 60
|
Db 8 ATGAGCTCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGG 67
|
Qy 61 GAAGTTGTGATGACTCAGTCTCACCTGCTCCCTCCCATCACACCTGGAGAGCGGCTCC 120
|
Db 68 GATGTTGTGATGACTCAGTCTCACCTGCTCCCTCCCATCACACCTGGAGAGCGGCTCC 127
|
Qy 121 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAAATGAGACACCTTCTGTGATGG 180
|
Db 128 ATCTCTGTAGTCTAGTCAAGCCTTCTGTATACAGTATGAAACACCTACTGATGG 187
|
Qy 181 TATCAGCAGAGCGGCGGCAACCTCCAAAGGCTCCTGATTTATAGGTTTCTAACCGGAC 240
|
Db 188 TTTACAGCAGAGCGGCGGCAACCTCCAAAGGCGCTAATTTATAGGTTTCTAACCGGAC 247
|
Qy 241 TCTGGGTTCCAGACAGATTCAGCGGAGTGGGCGGAGGACAGATTTTCACTGAAATC 300
|
Db 248 TCTGGGTTCCAGACAGATTCAGCGGAGTGGGCGGAGGACAGATTTTCACTGAAATC 307
|
Qy 301 AGCGCAGTGGAGGCTGAGATGTTGGGTTTATTTCTCGGCGCAAGGTACAGGACTCCT 360
|
Db 308 AGCAGGTTGGAGGCTGAGATGTTGGGTTTATTTCTGCTATGCAAGGTACACACTGGCCG 367
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:13:54 ; Search time 1370.41 Seconds
(without alignments)
8508.978 Million cell updates/sec

Title: US-09-758-173-5
Perfect score: 720
Sequence: 1 ATGAGCTCCTCTCAGCT.....TCAACAGGGAGAGTGTGA 720

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em_estba:*

2: em_esthum:*

3: em_estnu:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_esti:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pun:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	618.8	85.9	816	13	B1759427
2	610.6	84.8	774	13	BM007808
3	598.2	83.1	857	13	B1758820
4	597.2	82.9	918	12	BG681688
5	594.4	82.6	898	14	BQ708918
6	592.4	82.3	726	13	BM007723

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7	591.8	82.2	995	14	BQ712430
8	590.8	82.1	952	12	BG758592
9	587.2	81.6	720	13	B1768966
10	578.4	80.3	908	12	BG685179
11	578	80.3	859	12	BG758795
12	570.6	79.2	958	14	BQ709417
13	570.2	79.2	880	12	BG755003
14	567.4	78.8	701	12	BG547597
15	565.8	78.6	730	12	BG740066
16	564.6	78.4	730	13	B1837183
17	558.6	77.6	753	12	BG756401
18	557.2	77.4	880	12	BG757588
19	555.6	77.2	875	13	B1518518
20	554.8	77.1	907	14	BQ708655
21	553.6	76.9	710	13	B1908471
22	549.6	76.3	931	12	BG757255
23	547.4	76.0	696	13	B1838136
24	542.4	75.3	716	13	B1908319
25	542	75.3	912	12	BF974515
26	538.8	74.8	653	10	AW404795
27	538	74.7	770	12	BG530186
28	537.4	74.6	962	13	B1819546
29	537	74.6	877	13	B1837569
30	535.8	74.4	934	12	BF974268
31	532	73.9	811	13	B1818338
32	527	73.2	700	12	BG547577
33	512	71.1	709	12	BG757932
34	509.6	70.8	824	13	B1824708
35	505	70.1	990	13	B1838327
36	503	69.9	777	12	BG565315
37	497.8	69.1	735	12	BF238157
38	497.4	69.1	904	14	BQ711273
39	496.8	69.0	964	12	BG757678
40	492.6	68.4	689	14	BM768355
41	490.8	68.2	1075	12	BG758924
42	490.4	68.1	634	14	BM783161
43	490.4	68.1	923	14	BQ711051
44	489.4	68.0	683	12	BG745349
45	489.4	68.0	881	14	BQ709375

ALIGNMENTS

RESULT 1
B1759427
LOCUS B1759427 816 bp mRNA linear EST 25-SEP-2001
DEFINITION G03043095F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183446 5', mRNA sequence.
ACCESSION B1759427
VERSION B1759427.1 GI:15751005
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 816)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-x@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.lnl.gov
Plate: LINL11457 row: n column: 23
High quality sequence start: 2
High quality sequence stop: 814.
Location/Qualifiers

FEATURES


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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR KIMMUNOGLOBULIN V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 73 FRAMEWORK-2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 81 112 FRAMEWORK-3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 131 FRAMEWORK-4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 32.5%; Score 403.5; DB 1; Length 131;
Best Local Similarity 59.8%; Pred. No. 4.5e-26;
Matches 79; Conservative 20; Mismatches 32; Indels 1; Gaps 1;

Qy 1 MSLPAQLLGLLLLCVPGSGEVWMTQSLPITPGEPASISCRSSQSLKHNGDTPLSW 60
Db 1 METDTLLWVLLWVPGSTGNIVLTQSPASLAVSLGQRATISCRASESV-DSYGNFMHW 59

Qy 61 YQOKPGQPPRLLIYKVSNRDSCVPDRFSGGAGTDFTLKISAVEAEDVGVECGQGTTP 120
Db 60 YQOKPGQPPKLLIYLAASMLESGVPARTFSGSGRTDFTLTIDPVEADDAATYCCQNNEDP 119

Qy 121 PTFGGGTVKEIK 132
Db 120 WTFGGGTVKEIK 131

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Search completed: March 29, 2003, 09:11:14
Job time : 6.69846 secs

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RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RL cDNA probe.";
RN Nucleic Acids Res. 13:6531-6544 (1985).
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBSJ databases.
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DR EMBL; X02990; CAA26733.1; -.
DR PIR; A01905; K4H017.
DR HSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 133 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 33.1%; Score 411.5; DB 1; Length 134;
Best Local Similarity 61.4%; Pred. No. 1.1e-26;
Matches 82; Conservative 23; Mismatches 26; Indels 1; Gaps 1;

QY 1 MSLPAQLGLLLCVPGSSGEVNTQSLPLTPGEPASISCRSSQSLKHSNGD-TFLS 59
Db 1 MYLQTVFISLLISGAGDIVNTQSPDLSVLSGERATINCKSSQSLYSNNKLYLA 60
QY 60 WYQKFGPPRLLIYKVSNDGVPDRFSGSGAGTDTFLKISAVEADVGVYFCQGTRT 119
Db 61 WYQKFGPPKLLIYWASTRESGVPDRFSGSGAGTDTFLKISAVEADVGVYFCQYNNL 120
QY 120 PTFGGTKVEIKR 133
Db 121 PWTFGGKVEIKR 134

RESULT 14
KV2E_MOUSE
ID KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771 (1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Ball M., Potter M.;
RT "Mechanisms of antibody diversity; multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).
DR PIR; A01935; KVM5M6.
DR HSP; P01679; 2FBU.
DR InterPro; IPR003006; Ig_MHC.

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RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT Group A-streptococcal polysaccharide";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383 (1984).
CC -1. MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
DR PIR; A01912; KVM517.
DR HSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
DR Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 32.5%; Score 404; DB 1; Length 113;
Best Local Similarity 68.1%; Pred. No. 3.4e-26;
Matches 77; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 21 EVMVTQSLPLTPGEPASISCRSSQSLKHSNGD-TFLSWYQKFGPPRLLIYKVSND 80
Db 1 DIVMTQAVFNPVTLGTSASISCRSSKSLHSNGITYLYWYLDKPGSPQLLYQMSNLA 60
QY 81 SGVPDRFSGSGAGTDTFLKISAVEADVGVYFCQGTRTPTFGGKVEIKR 133
Db 61 SGVPDRFSGSGAGTDTFLKISAVEADVGVYCAHNLELPTVFGGKVEIKR 113

RESULT 15
KV3I_MOUSE
ID KV3I_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=981179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400 (1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771 (1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Ball M., Potter M.;
RT "Mechanisms of antibody diversity; multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).
DR PIR; A01935; KVM5M6.
DR HSP; P01679; 2FBU.
DR InterPro; IPR003006; Ig_MHC.

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Db 120 IPTFGGQTRVEIKR 133

RESULT 11

KV3H_HUMAN STANDARD; PRT; 129 AA.
 ID P04207;
 AC 20-MAR-1987 (Rel. 04, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86177570; PubMed=3083417;
 RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curo J.G., Chen P.P.,
 RA Goldfien R., Carson D.A.;
 RT "Cloning and sequence determination of a human rheumatoid factor
 RT light-chain gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M12740; AAAS8992.1; --
 DR PIR: A01898; K3HUC1.
 DR HSP: P80362; IWL.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; ig_1.
 DR SMART: SM00406; IGV; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 77 108 FRAMEWORK-3.
 FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 108 JK1 SEGMENT.
 FT NON TER 129 129 BY SIMILARITY.
 SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 33.3%; Score 414; DB 1; Length 129;
 Best Local Similarity 60.4%; Pred. No. 6.3e-27;
 Matches 81; Conservative 23; Mismatches 24; Indels 6; Gaps 2;
 QY 1 MSLPAQLGLLLCVPGSSGEVMTQSPSLPTTPGPASISCRSSQSLKXNGDTFLSW 60
 Db 1 MEAPQALLFLLLLWLPDITGEIVMTQSPATLSVSGPERATLSCRASQSVNN-----LAW 55
 QY 61 YQKPGPPRLLYKYVNSRDGVPDRFSGSGAGTDFTLKISAVEAEADVGYFCGQGRTP 120
 Db 56 YQKPGPPRLLYKYVNSRDGVPDRFSGSGAGTDFTLKISAVEAEADVGYFCGQGRTP 115
 QY 121 P-TFGGQTRVEIKR 133
 Db 116 PTFGGQTRVEIKR 129

RESULT 12

KV3M_HUMAN

KV3M_HUMAN STANDARD; PRT; 129 AA.
 ID P18136;
 AC 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region HIC precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kippes T.J., Tomhave E., Chen P.P., Carson D.A.;
 RA "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy."
 RL J. Exp. Med. 167:840-852(1988).
 CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC LEUKEMIA.
 CC AUTANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 DR PIR: P18021; K3HUH1.
 DR HSP: P80362; IWL.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; ig_1.
 DR SMART: SM00406; IGV; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 56 70 FRAMEWORK-2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 78 109 FRAMEWORK-3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 109 JK1 SEGMENT.
 FT NON TER 129 129 BY SIMILARITY.
 SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 33.3%; Score 414; DB 1; Length 129;
 Best Local Similarity 61.7%; Pred. No. 6.3e-27;
 Matches 82; Conservative 21; Mismatches 26; Indels 4; Gaps 1;
 QY 1 MSLPAQLGLLLCVPGSSGEVMTQSPSLPTTPGPASISCRSSQSLKXNGDTFLSW 60
 Db 1 MEAPQALLFLLLLWLPDITGEIVMTQSPATLSVSGPERATLSCRASQSVSS---YLAW 56
 QY 61 YQKPGPPRLLYKYVNSRDGVPDRFSGSGAGTDFTLKISAVEAEADVGYFCGQGRTP 120
 Db 57 YQKPGPPRLLYKYVNSRDGVPDRFSGSGAGTDFTLKISAVEAEADVGYFCGQGRTP 116
 QY 121 PTFGGQTRVEIKR 133
 Db 117 WTFGGQTRVEIKR 129

RESULT 13

KV4C_HUMAN

KV4C_HUMAN STANDARD; PRT; 134 AA.
 ID P06314;
 AC 01-JAN-1988 (Rel. 06, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-IV region B17 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041854; PubMed=2997713;
 QY 121 PTFGGQTRVEIKR 133
 Db 117 WTFGGQTRVEIKR 129

DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 44 55 FRAMEWORK-2.
 FT DOMAIN 56 70 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 71 77 FRAMEWORK-3.
 FT DOMAIN 78 109 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 110 118 JKI SEGMENT.
 FT DOMAIN 119 129 BY SIMILARITY.
 FT DISULFID 43 109
 FT NON TER 129 129
 SQ SEQUENCE 129 AA; 14073 MW; D3C552927772774D0 CRC64;
 Query Match 34.0%; Score 422; DB 1; Length 129;
 Best Local Similarity 62.4%; Pred. No. 1.4e-27;
 Matches 83; Conservative 21; Mismatches 25; Indels 4; Gaps 1;
 QY 1 MSLPAQLLGLLLCVPGSSGEVVMQPSLPTPGEPASISCRSSQSLKHSNGDFTLSW 60
 DB 1 METPAQLFLLLLPDPTTGIVLTQSGTSLSPGGERATLSGRASQSVSS---YLAW 56
 QY 61 YQOKPQPPRLIYKVSNRDGVDPFRSGSGAGTDFTLKISAVEAEDGVYFCGQGTTP 120
 DB 57 YQOKPQPPRLIYKVSNRDGVDPFRSGSGAGTDFTLKISAVEAEDGVYFCGQGTTP 116
 QY 121 PTFGGGTKEIKR 133
 DB 117 RTFGGGTKEIKR 129
 RESULT 9
 KV2A HUMAN STANDARD; PRT; 115 AA.
 AC P01614;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region Cum.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=68242259; PubMed=5586923;
 RA Hilschmann N.;
 RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
 RN [2]
 RP REVISIONS TO 50; 52; 95 AND 97.
 RX MEDLINE=70063440; PubMed=4188189;
 RA Hilschmann N.;
 RT "Molecular basis of antibody formation.";
 RL Naturwissenschaften 56:195-205(1969).
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01885; K2HUCM.
 DR HSSP; P01607; IREI.
 DR InterPro; IPR003006; IGV_MHC.
 DR InterPro; IPR003596; IGV_V.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 24 95
 FT NON TER 115 115
 SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;
 Query Match 33.9%; Score 420.5; DB 1; Length 115;
 Best Local Similarity 71.9%; Pred. No. 1.6e-27;
 Matches 82; Conservative 15; Mismatches 16; Indels 1; Gaps 1;

QY 21 EVVMTQPSLPLPTPGEPASISCRSSQSLKHS-NGDFTLSWYQKPGOPPLLIYKVSNR 79
 DB 2 DIVMTQPSLPLPTPGEPASISCRSSQSLSDGNGTNYLNWYLOKAGOSPOLLITLSYR 61
 QY 80 DSGVPRFRSGSGAGTDFTLKISAVEAEDGVYFCGQGTTPPTFGGGTKEIKR 133
 DB 62 ASGVPRFRSGSGAGTDFTLKISAVEAEDGVYFCGQGTTPPTFGGGTKEIKR 115
 RESULT 10
 KV4B HUMAN STANDARD; PRT; 133 AA.
 AC P06313;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-IV region JI precursor.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041853; PubMed=2997712;
 RA Klobbeck H.G.; Bornkamm G.W.; Combriato G.; Mocikat R.; Pohlenz H.D.;
 RA Zachau H.G.;
 RT "Subgroup IV of human immunoglobulin K light chains is encoded by a single germline gene.";
 RL Nucleic Acids Res. 13:6515-6529(1985).
 CC -----
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 CC -----
 DR EMBL; Z00022; CA477317.1; -.
 DR PIR; A01904; K4HUIJ.
 DR HSSP; P80362; IWTU.
 DR InterPro; IPR003006; IGV_MHC.
 DR InterPro; IPR003596; IGV_V.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 61 75 FRAMEWORK-2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 83 114 FRAMEWORK-3.
 FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 123 132 FRAMEWORK-4.
 FT DISULFID 43 114
 FT NON TER 133 133 BY SIMILARITY.
 SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;
 Query Match 33.8%; Score 420; DB 1; Length 133;
 Best Local Similarity 64.2%; Pred. No. 2.1e-27;
 Matches 86; Conservative 19; Mismatches 27; Indels 2; Gaps 2;
 QY 1 MSLPAQLLGLLLCVPGSSGEVVMQPSLPTPGEPASISCRSSQSLKHSNGDFTLSW 59
 DB 1 MVLQTVFTSLLSWISGAYGDIVMTQPSDLSVSLGERATINCKSSQSVLYSSNNKNYLA 60
 QY 60 YQOKPQPPRLIYKVSNRDGVDPFRSGSGAGTDFTLKISAVEAEDGVYFCGQGTTP 119
 DB 61 YQOKPQPPRLIYKVSNRDGVDPFRSGSGAGTDFTLKISAVEAEDGVYFCGQGTTP 119
 QY 120 PTFGGGTKEIKR 133

DE	Ig kappa chain V-II region FR.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=76253627; PubMed=821524;
RT	Riesen W.F., Jaton J.-C.;
RT	"Variable region sequence of the light chain from a Waldenstroms IgM
RL	with specificity for phosphorylcholine.";
RL	Biochemistry 15:3825-3833(1976)."
CC	-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC	MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
DR	PIR; A01886; K2HUFR.
DR	HSSP; P01607; 1REI.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_V.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGV; 1.
KW	Immunoglobulin V region.
FT	DOMAIN 1 23
FT	DOMAIN 24 39
FT	DOMAIN 40 54
FT	DOMAIN 55 61
FT	DOMAIN 62 93
FT	DOMAIN 94 102
FT	DOMAIN 103 112
FT	DISULFID 23 93
FT	NON_TER 113 113
SQ	SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;
Query Match	34.6%; Score 430; DB 1; Length 113;
Best Local Similarity	71.7%; Pred.No. 2.7e-28;
Matches 81; Conservative	13; Mismatches 19; Indels 0; Gaps
QY	21 EVVMQTSPSLPTTPEGPASICSRSSQSLSKHSGDTFLSWYQQKQPPLRIYKVSNRD 80
Db	1 DVVMTQSPFLPVLTGEPASIQCRSSQSLVVRGGTYLBWYLKPGQSPPELLIYLSSYRD 60
::: ::: ::: ::: ::: ::: ::: :::	
QY	81 SGVPDFSGSGAGDTFTLKISAEVAEDVGYYFCQGTRTPPTFGGTKEIKR 133
Db	61 SGVPDFDSGSGTGDTFTLKIRVOAEDVGYYVCQATZSPYTFGQTKLZIKR 113
::: ::: ::: ::: ::: ::: :::	
 RESULT 8 KV3L_HUMAN KV3L_HUMAN STANDARD; PRT; 129 AA. AC F18135; DT 01-NOV-1990 (Rel. 16, Created) DT 01-NOV-1990 (Rel. 16, Last sequence update) DT 15-JUL-1999 (Rel. 38, Last annotation update) DT IG kappa chain V-III region HAH precursor. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. RX MEDLINE=88171307; PubMed=3127527; RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;	
RT	"Antibody-associated kappa light chain variable region gene
RT	expressed in chronic lymphocytic leukemia with little or no somatic
RT	mutation. Implications for etiology and immunotherapy.";
CC	J. Exp. Med. 167:840-852(1988).
CC	-!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC	AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC	LEUKEMIA.
DR	PIR; P10022; K3UHA.
DR	HSSP; P80362; IWTL.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_V.
DR	Pfam; PF00047; ig; 1.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z00009; -; NOT ANNOTATED_CDS.
CC PIR; A01889; K2HUTW.
CC HSSP; P80362; LWTL.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC Immunoglobulin V region; Signal.
CC NON_TER 1 4
CC SIGNAL <1 4
CC CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
CC DOMAIN 5 27 FRAMEWORK-1.
CC DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 44 58 FRAMEWORK-2.
CC DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 66 97 FRAMEWORK-3.
CC DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.
CC DOMAIN 107 116 FRAMEWORK-4.
CC DISULFID 27 97 BY SIMILARITY.
CC NON_TER 117 117
CC SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 39.2%; Score 487; DB 1; Length 117;
Best Local Similarity 80.3%; Pred. No. 7e-33;
Matches 94; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 17 GSSEVVMQSPSLPITGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKV 76
DB 1 GSSGDIWMTQSPSLPVTGEPASISCRSSQSLHSGNYLDWYKQKPGQSPQLLIYIG 60

QY 77 SNRDSGVPRFSGSGAGTDTFLKISAVEAEDVGVPFCGGGTPTPTFGGKTVEIKR 133
DB 61 SNRAGVPRFSGSGGTDFTLKISRVEAEDGVPYVCMQGLQTPPTFGGKTVEIKR 117

RESULT 4
KV2G MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody.";
RL BiochemJ 22:1153-1158(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
CC PROTEIN THAT BINDS DIGOXIN.
CC PIR; A01914; KVM26.
CC HSSP; P80362; LWTL.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC Immunoglobulin V region; Monoclonal antibody; Hybridoma.

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FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 37.9%; Score 471; DB 1; Length 113;
Best Local Similarity 77.9%; Pred. No. 1.3e-31;
Matches 88; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 21 EVVMTQSPSLPITGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVNRD 80
DB 1 DVVMTQSPSLPVSIGDQASISCRSSQSLVHSGNTYLNWYKQKPGQSPKLLIYKVNRF 60

QY 81 SGVPRFSGSGAGTDTFLKISAVEAEDVGVPFCGGGTPTPTFGGKTVEIKR 133
DB 61 SGVPRFSGSGGTDFTLKISRVEAEDGVPYVCMQGLQTPPTFGGKTVEIKR 113

RESULT 5
KV2D HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
primary amyloidosis.";
RL Biochemistry 12:3763-3780(1973).
RN [2]
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=73166638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
RA Glenner G.G.;
RA "Structural identity of Bence Jones and amyloid fibril proteins in a
patient with plasma cell dyscrasia and amyloidosis.";
RL J. Clin. Invest. 52:1276-1281(1973).
CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSKRASIA AND AMYLOIDOSIS.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC PIR; A01888; K2HUTW.
CC HSSP; P01607; IREI.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC Immunoglobulin V region; Bence-Jones protein; Amyloid.
CC DOMAIN 1 23 FRAMEWORK-1.
CC DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 40 54 FRAMEWORK-2.
CC DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 62 93 FRAMEWORK-3.
CC DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
CC DOMAIN 103 112 FRAMEWORK-4.
CC DISULFID 23 93 BY SIMILARITY.
CC NON_TER 113 113

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QY 61 YQKPGQPPRLIIKYKSNRDSGVDPFSGSGAGTDTFTLKISAVEADVGIVFCQGTRTP 120
 Db 61 FQKPGQSPRLIIKYKSNRDSGVDPFSGSGAGTDTFTLKISAVEADVGIVFCQGHWS 120
 QY 121 PTFGGGTTKVEIKR 133
 Db 121 WTFGGGTTKVEIKR 133

RESULT 2
 KAC_HUMAN STANDARD; PRT; 106 AA.
 AC P01834;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig kappa chain C region.
 GN IGKC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (MYELOMA PROTEIN EU).
 RX MEDLINE=71064023; PubMed=5489770;
 RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
 acid sequence of the light chain."
 RL Biochemistry 9:3155-3161(1970).
 RN [2]
 RP DISULFIDE BONDS.
 RX MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 Intra-chain disulfide bonds."
 RL Biochemistry 9:3188-3196(1970).
 RN [3]
 RP SEQUENCE (BENCE-JONES PROTEIN TI).
 RX MEDLINE=72188439; PubMed=5027703;
 RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
 TI). IV. The complete amino acid sequence and its significance for
 the mechanism of antibody production."
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81042304; PubMed=6775818;
 RA Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;
 RT "Cloned human and mouse kappa immunoglobulin constant and J region
 genes conserve homology in functional segments."
 RL Cell 22:197-207(1980).
 RN [5]
 RP SEQUENCE (BENCE-JONES PROTEIN ROY).
 RX Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;
 RL (In) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press,
 RL New York (1969).
 RN [6]
 RP SEQUENCE (BENCE-JONES PROTEIN CUM).
 RX MEDLINE=68242259; PubMed=5586923;
 RA Hilschmann N.;
 RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
 type)."
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
 RN [7]
 RP SEQUENCE (BENCE-JONES PROTEIN AG).
 RX MEDLINE=69234734; PubMed=4893682;
 RA Titani K., Shinoda T., Putnam F.W.;
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
 complete sequence and the location of the disulfide bridges."

J. Biol. Chem. 244:3550-3560(1969).
 RN [8]
 RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
 RX MEDLINE=70201507; PubMed=5447531;
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
 RT "Macroglobulin structure: variable sequence of light and heavy
 chains."
 RL Science 169:56-59(1970).
 CC -|- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
 CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
 CC MARKER, 45-ALA AND 83-LEU.
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 CC -----
 CC EMBL; J00241; AAA58989.1; -
 DR EMBL; V00557; CAA23823.1; -
 DR PIR; A02116; K3HU.
 DR HSSP; P01842; 7FAB.
 DR Genew; HGNC:5716; IGKC.
 DR MIM; 147200; -
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_c1.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00407; IGc1; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DISULFID 26 86
 FT DISULFID 106 106
 FT VARIANT 83 83
 FT INTERCHAIN (WITH A HEAVY CHAIN).
 FT V -> L (IN INV(1,2) MARKER).
 FT /FTID=VAR_003897.
 FT CONFLICT 14 14 D -> N (IN REF. 7 AND 8).
 FT CONFLICT 57 57 E -> Q (IN REF. 5 AND 6).
 FT CONFLICT 57 57 E -> Q (IN REF. 5 AND 6).
 SQ SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;
 Query Match 44.1%; Score 548; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred. No. 7.2e-38;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 134 TVAAPSVFIFPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 193
 Db 1 TVAAPSVFIFPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60
 QY 194 KOSTYSLSTLTSLKADYKHKYKACEVTHQGLSSPVTKSPNRGEC 239
 Db 61 KOSTYSLSTLTSLKADYKHKYKACEVTHQGLSSPVTKSPNRGEC 106
 RESULT 3
 KV2E_HUMAN STANDARD; PRT; 117 AA.
 ID KV2E_HUMAN
 AC P06309;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region GM607 precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84191506; PubMed=6325927;
 RA Klobbeck H.G., Solomon A., Zachau H.G.;
 RT "Contribution of human V kappa II germ-line genes to light-chain
 RT diversity."
 RL Nature 309:73-76(1984).

GenCore version 5.1.4.p5 4578
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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 5.69846 Seconds
(without alignments)
1739.566 Million cell updates/sec

Title: US-09-758-173-6

Perfect score: 1242

Sequence: 1 MSLLPAQLGLLLCVPGSSG.....EVTHQGLSSPVTKSFNRGEC 239

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	550	44.3	133	1 KV2F_HUMAN	P06310 homo sapien
2	548	44.1	106	1 KAC_RAT	P01834 homo sapien
3	487	39.2	117	1 KV2E_HUMAN	P06309 homo sapien
4	471	37.9	113	1 KV2F_MOUSE	P01631 mus musculus
5	453	36.5	113	1 KV2D_HUMAN	P01617 homo sapien
6	433.5	34.9	112	1 KV2C_HUMAN	P01616 homo sapien
7	430	34.6	113	1 KV2B_HUMAN	P01615 homo sapien
8	422	34.0	129	1 KV3L_HUMAN	P18135 homo sapien
9	420.5	33.9	115	1 KV2A_HUMAN	P01614 homo sapien
10	420	33.8	133	1 KV4B_HUMAN	P06313 homo sapien
11	414	33.3	129	1 KV3H_HUMAN	P04207 homo sapien
12	414	33.3	129	1 KV3M_HUMAN	P18136 homo sapien
13	411.5	33.1	134	1 KV4C_HUMAN	P06314 homo sapien
14	404	32.5	113	1 KV2E_MOUSE	P03976 mus musculus
15	403.5	32.5	131	1 KV3I_MOUSE	P01661 mus musculus
16	401	32.3	131	1 KV2F_MOUSE	P01630 mus musculus
17	399.5	32.2	132	1 KV3F_MOUSE	P01658 mus musculus
18	396.5	31.9	128	1 KV3D_HUMAN	P06311 homo sapien
19	389	31.3	112	1 KV2D_HOUSE	P01625 mus musculus
20	384.5	31.0	114	1 KV4A_HUMAN	P01624 mus musculus
21	372.5	30.0	115	1 KV3I_HUMAN	P04433 homo sapien
22	372	30.0	109	1 KV3D_HUMAN	P01622 homo sapien
23	369.5	29.8	121	1 KV4O_HUMAN	P06312 homo sapien
24	368.5	29.7	111	1 KV3H_MOUSE	P01660 mus musculus
25	368.5	29.7	136	1 KV5B_MOUSE	P01634 mus musculus
26	368	29.6	113	1 KV2C_MOUSE	P01628 mus musculus
27	367	29.5	106	1 KAC_RAT	P01835 rattus norv
28	364.5	29.3	111	1 KV3M_MOUSE	P01665 mus musculus
29	364.5	29.3	111	1 KV3O_MOUSE	P01667 mus musculus
30	364	29.3	109	1 KV3B_HUMAN	P01620 homo sapien
31	364	29.3	120	1 KV2B_MOUSE	P01627 mus musculus
32	363.5	29.3	111	1 KV3N_MOUSE	P01666 mus musculus
33	361	29.1	109	1 KV3F_HUMAN	P01624 homo sapien

34	359.5	28.9	108	1 KVI_CANFA	P01618 canis famil
35	359	28.9	106	1 KAC_RAT	P01836 rattus norv
36	358.5	28.9	111	1 KV3J_MOUSE	P01662 mus musculus
37	358	28.8	110	1 KV3P_MOUSE	P01668 mus musculus
38	357.5	28.8	111	1 KV3C_MOUSE	P01656 mus musculus
39	357.5	28.8	111	1 KV3Q_MOUSE	P01669 mus musculus
40	356.5	28.7	111	1 KV3T_MOUSE	P01672 mus musculus
41	354.5	28.5	111	1 KV3L_MOUSE	P01664 mus musculus
42	354.5	28.5	111	1 KV3R_MOUSE	P01670 mus musculus
43	354.5	28.5	129	1 KVI_HUMAN	P04431 homo sapien
44	354	28.5	109	1 KV3E_HUMAN	P01623 homo sapien
45	353	28.4	112	1 KV2A_MOUSE	P01626 mus musculus

ALIGNMENTS

RESULT 1
KV2F_HUMAN
ID_KV2F_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Last Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Weindl A., Combrato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and III";
RL Nucleic Acids Res. 13:6499-6513 (1985).
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EMBL; Z00020; CAA77315.1; -
PIR; A01890; K2HURP.
HSSP; P80362; 1WTL.
InterPro; IPR003006; Iq_MHC.
InterPro; IPR003596; Iq_v.
Pfam; PF00047; Iq; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
SIGNAL 1 20
CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 60 74 FRAMEWORK-2.
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 82 113 FRAMEWORK-3.
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 113 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 44.3%; Score 550; DB 1; Length 133;
Best local Similarity 80.5%; Pred. No. 6.6e-38;
Matches 107; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

Oy 1 MSLLPAQLGLLLCVPGSSGVVMTQSPVLSPTTPEGPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MSLLPAQLGLLLCVPGSSGVVMTQSPVLSPTTPEGPASISCRSSQSLVSDGNTYLNW 60

Best Local Similarity 61.4%; Pred. No. 2.1e-42;
Matches 135; Conservative 34; Mismatches 50; Indels 1; Gaps 1;

Qy 21 EYVMTQSPLSPITGPEPASISCRSSQLKHSNGD-TFLSWTQQKPGOPPRLLIYKVSNR 79
::||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 DIVMTQSPSSLTVTAGKVTWMSCTSSQSLFNSGKNLYLWYQQKFGOPPVLIIWASTR 60
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 80 DSGVPDRFSGGAGDTFTLKISAVEAEDGVVFYCGQGRTPPTFGGTGKVKIKRTVAAPS 139
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 ESGVPDRFTSGSGDFTLTISSVQAEDLAVVYCNDYSNPLTFGGGTGKLEKRAAAAPT 120
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 140 VFIPPSDEQLKSQTASVVCLLNPFYPREAKVQWKVDNALSGNSQS SVTTQDSKDSTYS 199
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 VSIFFPSEQLTSGGASVVCFLNNFPYKDIINVKWIDSERQNGVLSNWTQDSKDSTYS 180
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 200 LSSLTLLSKADYEKKHKVACEVTHOGLSPPVTKSFNRGEC 239
:||||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 191 MSSLTLLTKDEYERNHNTCEATHKTSTSPIVKSFNREC 220
:||||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 14
S37484
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C:Accession: S37484
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37484
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-225 <DUC>
A:Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 56.5%; Score 702; DB 2; Length 225;
Best Local Similarity 58.5%; Pred. No. 6.1e-41;
Matches 134; Conservative 37; Mismatches 52; Indels 6; Gaps 2;

Qy 11 LLLCPVGSSGVVMTQSPSLPIPTGPASPISCRSSQLKHISNGDFTLSWYQQKPGQPPR 70
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 LLLCVSAHGSGIVMTQTPKFLLSAGDRVITTCASQSVSND----VAMYQQKPGQSPK 57
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 71 LLIVKYNRDGSDVRFSGSGAGDTFTLKISAVEAEDGVVFYCGQGRTPPTFGGTGKVE 130
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 58 LLIVYASRYTGVPDRFTSGSGDGTDFTTISTVQAEDLAVFYC-QDYSSYTFGGGTGLE 116
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 131 IKRTVAAPSVFIPPSPDEQLKSQTASVVCLLNPFYPREAKVQWKVDNALSGNSQS SVTE 190
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 117 IKRDAAPTYSIFPPSPDEQLTSGGASVVCFLNNFPYKDIINVKWIDSERQNGVLSNWT 176
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 191 QDSKDSTYSLSSTLTLKADYEKKHKVACEVTHOGLSPPVTKSFNRGEC 239
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 177 QDSKDSTYSMSSTLLTKDEYERNHNTCEATHKTSTSPIVKSFNREC 225
||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
S68241
Ig kappa chain V region (Mab13-1) - mouse (fragment)
N:Alternate names: immunoglobulin light chain
C:Species: Mus musculus (house mouse)
C>Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68241; S68214
R:Takagi, M.; Konda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imoto
submitted to the EMBL Data Library, March 1994
A:Description: Specific peroxidase activity by formation of an antibody L-chain
A:Reference number: S68241
A:Accession: S68241
A:Molecule type: mRNA
A:Residues: 1-218 <TAKE>
A:Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963

```
RESULT 10
S42772
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42772
R:Schellekens, G.A.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42771
A:Accession: S42772
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <SCH>
A:Cross-references: EMBL:X75536; NID:g414143; PIDN:CAA53226.1; PID:g414144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:14-93/Domain: immunoglobulin homology <IMM>

Query Match 64.0%; Score 795; DB 2; Length 217;
Best Local Similarity 68.7%; Pred. No. 2.8e-47;
Matches 149; Conservative 26; Mismatches 42; Indels 0; Gaps 0;

QY 23 VMTQSLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIYKVNRSRG 82
Db 1 VMTQSLSLPVLGDAQASISCRSSQSLVHTNGNTYLHWYQKPGQSPKVLIVKVSSTRESG 60

QY 83 VPRFSGSGAGTDFTLKISAVEAEDVGVYFCGGQTRTPPTFGGGTKVEIKRTVAAPSVFI 142
Db 61 VPRFSGSGSGTDFTLKISAVEAEDLGVYFCQSQTVVPTFGSGTKLEIKRADAAFTVSI 120

QY 143 PPSDEQLKGTASVCLNNFYPRKAVQKVDNALQSGNSQESVTEQDSKDYSLSS 202
Db 121 PPSSEQLTSGGASVCLNNFYPRKAVQKVDNALQSGNSQESVTEQDSKDYSLSS 180

QY 203 TLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 239
Db 181 TLTLYKDEYERHNSYTCETHTKTSTSPVTKSFNRGEC 217

RESULT 11
JL0029
Ig kappa chain precursor (RP93) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
C:Accession: JL0029
R:Chien, N.C.; Pollock, R.R.; Desaymard, C.; Scharff, M.D.
J. Exp. Med. 167, 954-973, 1988
A:Title: Point mutations cause the somatic diversification of IgM and IgG2a anti-phospho-
A:Reference number: JL0029; MUID:88171315; PMID:3127529
A:Accession: JL0029
A:Molecule type: mRNA
A:Residues: 1-225 <CHI>
A:Experimental source: strain BALB/c, cell line RP93 hybridoma cell
A:Note: the authors translated the codon CGG for residue 106 as Pro, ACC for residue 132
A:Note: the nucleotide sequence shown is inconsistent with authors' translation because
ect except for four positions shown above
C:Comment: The protein is an anti-phosphorylcholine antibody.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:7-225/Product: Ig kappa chain #status predicted <ILC>
F:7-106/Domain: V region #status predicted <VAB>
F:107-119/Domain: J region #status predicted <ILR>
F:120-225/Domain: C region #status predicted <COR>

Query Match 62.0%; Score 770; DB 2; Length 225;
Best Local Similarity 64.7%; Pred. No. 1.5e-45;
Matches 143; Conservative 32; Mismatches 46; Indels 0; Gaps 0;

QY 19 SGEVMTQSLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIYKVN 78
Db 5 SSDVLATQIPLSLVLGDAQASISCRSSQSLVHTNGNTYLHWYQKPGQSPKVLIVKISN 64
```

```
QY 79 RDSGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGGQTRTPPTFGGGTKVEIKRTVAAP 138
Db 65 RFSGVDPDRFSGSGSGTDFSLKISAVEAEDLGVYCYCQSSHVRWTFGGGTLKLEIKRADAAP 124

QY 139 SVTFPPSDQLKGTASVCLNNFYPRKAVQKVDNALQSGNSQESVTEQDSKDYSLSS 198
Db 125 TVSIPTPTSLTSGGASVCLNNFYPRKAVQKVDNALQSGNSQESVTEQDSKDYSLSS 184

QY 199 SLSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 239
Db 185 SMSSTLTLYKDEYERHNSYTCETHTKTSTSPVTKSFNRGEC 225

RESULT 12
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA.
A:Reference number: S06084; MUID:90016888; PMID:2508067
A:Accession: S06084
A:Molecule type: mRNA
A:Residues: 1-240 <CRO>
A:Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-240/Domain: signal sequence #status predicted <SIG>
F:21-240/Product: Ig kappa chain #status predicted <MAT>
F:153-222/Domain: immunoglobulin homology <IMM>

Query Match 61.6%; Score 765.5; DB 2; Length 240;
Best Local Similarity 61.7%; Pred. No. 3.1e-45;
Matches 148; Conservative 34; Mismatches 57; Indels 1; Gaps 1;

QY 1 MSLPAOLLGULLLVCVSGSSEVMTQSLSLPITPGEPASISCRSSQSLKHS-NGDTFLS 59
Db 1 MESQTQVLMSLLLWISGTCGDFVMTQSPSLAVSAGETVTINCKSSQSLFYSGNKVYLA 60

QY 60 WYQKFGQPPRLIYKVNRSRGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGGQTRT 119
Db 61 WYQKFGQSPKLLIYWASPTQSGVDPDRFSGSGAGTDFTLTSSVQAEALAIYCLQYET 120

QY 120 PTFGGGTKVEIKRTVAAPSVFIPTPSDEQLKGTASVCLNNFYPRKAVQKVDNAL 179
Db 121 PTFGGAGTKLEIKRADAAPTIVSIFPSTEQATGATGASVCLNNFYPRDISVKWKIDGTE 180

QY 180 QSGNSQESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 239
Db 181 RRDGVLDSTVDQDSKDYSLSSMTSLSLKADYKHKVYACEVTHQGLSPVTKSFNRGEC 240

RESULT 13
A31790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an ant
A:Reference number: A92686; MUID:89034213; PMID:3182835
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: GB:W23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 58.3%; Score 723.5; DB 2; Length 220;
```

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <VAN>
A:Cross-references: EMBL:L35138; NID:G522336; PIDN:AAA67525.1; PID:G522337
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 66.0%; Score 820; DB 2; Length 219;
Best Local Similarity 69.4%; Pred. No. 5.6e-49;
Matches 152; Conservative 28; Mismatches 39; Indels 0; Gaps 0;
QY 21 EVVMTQSLPLPITGEPASISCRSSQSLKHSNGDTFLSWYQKPGOPPLLIYKVSNRD 80
DB 1 DVVMTQSLPLPVSIGDQASISCRSSQSLVHSGNTLYLWYKPGQSPKLLIYVSNRF 60
QY 81 SGVPRFSGSGAGDTFTLKISAVEADVGYYFCGGGTRPTFTFGGTVKIKRTVAAPSV 140
DB 61 SGVPRFSGSGGTDFTLKISRVEAEDLGVYFCGSHVPTFTFGGTVNLEIKRADAAPT 120
QY 141 FIFPPSDEQLKSGTASVCLLNFPYKQWVDNALQSGNSQESVTEQDSKDSYSTL 200
DB 121 SIFPPSSEQLTSGGASVVCFLNFPKDIIVKWIDGSEKQNGVLSWNTDQDSKDSYSTM 180
QY 201 SSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 239
DB 181 SSTLTLTCKDEYERHNSYTCATHKTSPIVKSFNREK 219

RESULT 7

PC4203
Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C:Accession: PC4203
R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a monoclonal antibody Maba34
A:Reference number: PC4202; MUID:97082978; PMID:8964510
A:Accession: PC4203
A:Molecule type: mRNA
A:Residues: 1-219 <KWA>
A:Cross-references: GB:U29147; NID:G1594225; PIDN:AAC52821.1; PID:G1594226
C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density lipoprotein (HDL)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:1-112/Domain: V region #status predicted <VRG>
F:113-219/Domain: C region #status predicted <CRG>

Query Match 65.0%; Score 807; DB 2; Length 219;
Best Local Similarity 68.0%; Pred. No. 4.3e-48;
Matches 149; Conservative 31; Mismatches 39; Indels 0; Gaps 0;
QY 21 EVVMTQSLPLPITGEPASISCRSSQSLKHSNGDTFLSWYQKPGOPPLLIYKVSNRD 80
DB 1 DVVMTQSLPLPVSIGDQASISCRSSQSLVHSGNTLYLWYKPGQSPKLLIYVSNRF 60
QY 81 SGVPRFSGSGAGDTFTLKISAVEADVGYYFCGGGTRPTFTFGGTVKIKRTVAAPSV 140
DB 61 SGVPRFSGSGGTDFTLKISRVEAEDLGVYFCGSHVPTFTFGGTVNLEIKRADAAPT 120
QY 141 FIFPPSDEQLKSGTASVCLLNFPYKQWVDNALQSGNSQESVTEQDSKDSYSTL 200
DB 121 SIFPPSSEQLTSGGASVVCFLNFPKDIIVKWIDGSEKQNGVLSWNTDQDSKDSYSTM 180
QY 201 SSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 239
DB 181 SSTLTLTCKDEYERHNSYTCATHKTSPIVKSFNREK 219

RESULT 8

S16112
Ig kappa chain V region (G2a) - mouse
C:Species: Mus musculus (house mouse)

C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16112
R:Vaesen, M.; Prosch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D.; F. Bol. Chem. Hoppe-Seyler 372, 451-453, 1991
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha(2-macroglobulin)
A:Reference number: S16112; MUID:92000313; PMID:1910583
A:Accession: S16112
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-219 <BIT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 64.9%; Score 806; DB 2; Length 219;
Best Local Similarity 68.9%; Pred. No. 5e-48;
Matches 151; Conservative 28; Mismatches 40; Indels 0; Gaps 0;
QY 21 EVVMTQSLPLPITGEPASISCRSSQSLKHSNGDTFLSWYQKPGOPPLLIYKVSNRD 80
DB 1 DVVMTQSLPLPVSIGDQASISCRSSQSLVHSGNTLYLWYKPGQSPKLLIYVSNRF 60
QY 81 SGVPRFSGSGAGDTFTLKISAVEADVGYYFCGGGTRPTFTFGGTVKIKRTVAAPSV 140
DB 61 SGVPRFSGSGGTDFTLKISRVEAEDLGVYFCGTHVPTFTFGGTVNLEIKRADAAPT 120
QY 141 FIFPPSDEQLKSGTASVCLLNFPYKQWVDNALQSGNSQESVTEQDSKDSYSTL 200
DB 121 SIFPPSSEQLTSGGASVVCFLNFPKDIIVKWIDGSEKQNGVLSWNTDQDSKDSYSTM 180
QY 201 SSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 239
DB 181 SSTLTLTCKDEYERHNSYTCATHKTSPIVKSFNREK 219

RESULT 9

S38865
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C:Accession: S38865
R:Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A:Description: Combination of a defined specificity and desired isotype by cloning of an antibody gene
A:Reference number: S38864
A:Accession: S38865
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <KIP>
A:Cross-references: EMBL:Z27396; NID:G416538; PIDN:CAA81787.1; PID:G416539
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 64.1%; Score 796; DB 2; Length 219;
Best Local Similarity 68.9%; Pred. No. 2.4e-47;
Matches 151; Conservative 26; Mismatches 42; Indels 0; Gaps 0;
QY 21 EVVMTQSLPLPITGEPASISCRSSQSLKHSNGDTFLSWYQKPGOPPLLIYKVSNRD 80
DB 1 ELVMTQSLPLPVSIGDQASISCRSSQSLVHSGNTLYLWYKPGQSPKLLIYVSNRF 60
QY 81 SGVPRFSGSGAGDTFTLKISAVEADVGYYFCGGGTRPTFTFGGTVKIKRTVAAPSV 140
DB 61 SGVPRFSGSGGTDFTLKISRVEAEDLGVYFCVQVTHVPTFTFGGTVNLEIKRADAAPT 120
QY 141 FIFPPSDEQLKSGTASVCLLNFPYKQWVDNALQSGNSQESVTEQDSKDSYSTL 200
DB 121 SIFPPSSEQLTSGGASVVCFLNFPKDIIVKWIDGSEKQNGVLSWNTDQDSKDSYSTM 180
QY 201 SSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 239
DB 181 SSTLTLTCKDEYERHNSYTCATHKTSPIVKSFNREK 219

Query Match 73.1%; Score 908; DB 2; Length 215;
 Best Local Similarity 79.9%; Pred. No. 5.7e-55;
 Matches 175; Conservative 19; Mismatches 21; Indels 4; Gaps 1;

Qy 21 EVVMTQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKQPGQPPRLIIYKVNRD 80
 Db 1 EIVLTQSPGTLSPGERATLSRASQSVNN---YLAWYQKQPGQAPSLIIYDASSRA 56
 Qy 81 SGVPDRFSGSGAGTDFTLKISAVEAEADVGVYFCGQGRTPPTFGGKVEIKRTVAAPSV 140
 Db 57 TGIPIRFSGSGGTDFTLTISGLEPDAVYICQYDRPWTPTFGQKVEIKRTVAAPSV 116
 Qy 141 FIPPPDEQLKSGTASVCLNNFYPRKAVQKVDNALQSGNSQSVTEQDSKDYSL 200
 Db 117 FIPPPDEQLKSGTASVCLNNFYPRKAVQKVDNALQSGNSQSVTEQDSKDYSL 176
 Qy 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
 Db 177 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 3
 JE0243
 Ig kappa chain NIG93 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: JE0243
 R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
 submitted to JIPID, November 1998
 A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy
 A:Reference number: JE0243
 A:Accession: JE0243
 A:Molecule type: protein
 A:Residues: 1-215 <ALI>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 70.5%; Score 876; DB 2; Length 215;
 Best Local Similarity 77.7%; Pred. No. 8.5e-53;
 Matches 171; Conservative 18; Mismatches 25; Indels 6; Gaps 2;

Qy 21 EVVMTQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKQPGQPPRLIIYKVNRD 80
 Db 1 EIVMTQSPATLSVSPGERATLSRASQSVN---TNVVMYQKQPGQAPRLIIYDASTRA 55
 Qy 81 SGVPDRFSGSGAGTDFTLKISAVEAEADVGVYFCGQGRTPPTFGGKVEIK-RTVAAPS 139
 Db 56 TGVPAFSGSGGTEFTLTISLSQSEDAIYICQHNNAWPTPTFGQKVEIKRTVAAPS 115
 Qy 140 VFIPPPDEQLKSGTASVCLNNFYPRKAVQKVDNALQSGNSQSVTEQDSKDYSL 199
 Db 116 VFIPPPDEQLKSGTASVCLNNFYPRKAVQKVDNALQSGNSQSVTEQDSKDYSL 175
 Qy 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
 Db 176 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 4
 A23746
 Ig kappa chain V-III (KAU cold agglutinin) - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
 C:Accession: A23746
 R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
 J. Biol. Chem. 266, 2836-2842, 1991
 A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
 A:Reference number: A23746; MUID:91131575; PMID:1993660
 A:Accession: A23746
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-215 <LEO>

C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 860; DB 2; Length 215;
 Best Local Similarity 78.4%; Pred. No. 1e-51;
 Matches 171; Conservative 18; Mismatches 25; Indels 4; Gaps 1;

Qy 21 EVVMTQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKQPGQPPRLIIYKVNRD 80
 Db 1 EIVLTQSPATLSVSPGERATLSRASQSVN---SSNYLAWYQKQPGQAPRLIIYDASSRA 56
 Qy 81 SGVPDRFSGSGAGTDFTLKISAVEAEADVGVYFCGQGRTPPTFGGKVEIKRTVAAPSV 140
 Db 57 TGIPIRFSGSGGTDFTLTISGLEPDAVYICQYDRPWTPTFGQKVEIKRTVAAPSV 116
 Qy 141 FIPPPDEQLKSGTASVCLNNFYPRKAVQKVDNALQSGNSQSVTEQDSKDYSL 200
 Db 117 FIPPPDEQLKSGTASVCLNNFYPRKAVQKVDNALQSGNSQSVTEQDSKDYSL 176
 Qy 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 177 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 5
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 Ig kappa chain Am37 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: JE0241
 R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
 submitted to JIPID, November 1998
 A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mult
 A:Reference number: JE0241
 A:Accession: JE0241
 A:Molecule type: protein
 A:Residues: 1-216 <ALI>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 67.8%; Score 841.5; DB 2; Length 216;
 Best Local Similarity 76.7%; Pred. No. 1.9e-50;
 Matches 168; Conservative 21; Mismatches 27; Indels 3; Gaps 3;

Qy 21 EVVMTQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKQPGQPPRLIIYKVNRD 80
 Db 1 DIVLTQSPDPLAVSLGERATINCKSQSVLY-NSKNFLAWYQKQPGQ-PKLLIW-ANVRE 57
 Qy 81 SGVPDRFSGSGAGTDFTLKISAVEAEADVGVYFCGQGRTPPTFGGKVEIKRTVAAPSV 140
 Db 58 SGVPDRFSGSGGTDFTLTISNQLAVYICQYDRPWTPTFGGKVEIKRTVAAPSV 117
 Qy 141 FIPPPDEQLKSGTASVCLNNFYPRKAVQKVDNALQSGNSQSVTEQDSKDYSL 200
 Db 118 FIPPPDEQLKSGTASVCLNNFYPRKAVQKVDNALQSGNSQSVTEQDSKDYSL 177
 Qy 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
 Db 178 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 216

RESULT 6
 S52028
 Ig kappa chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C:Accession: S52028
 R:van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkae, W.G.; Schots, A.; I
 submitted to the EMBL Data Library, August 1994
 A:Description: Coordinates expression of antibody subunit genes yields high levels of func
 A:Reference number: S52028
 A:Accession: S52028

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:24 ; Search time 10.7265 Seconds
(without alignments)
2141.995 Million cell updates/sec

Title: US-09-758-173-6

Perfect score: 1242

Sequence: 1 MSLLPAQLGLLLLCVPGSSG.....EVTHQGLSSPVTKSFNRGEC 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	915	73.7	215	2 JE0244	Ig kappa chain NIG
2	908	73.1	215	2 JE0242	Ig kappa chain NIG
3	876	70.5	215	2 JE0243	Ig kappa chain NIG
4	860	69.2	215	2 A23746	Ig kappa chain V-I
5	841.5	67.8	216	2 JE0241	Ig kappa chain Am3
6	820	66.0	219	2 S2028	Ig kappa chain - m
7	807	65.0	219	2 PC4203	Ig kappa chain (no
8	806	64.9	219	2 S16112	Ig kappa chain v r
9	796	64.1	219	2 S38865	Ig kappa chain - m
10	795	64.0	217	2 S42772	Ig kappa chain - m
11	770	62.0	225	2 JL0029	Ig kappa chain pre
12	765.5	61.6	240	2 SC06084	Ig kappa chain pre
13	723.5	58.3	220	2 A31290	Ig kappa chain v r
14	702	56.5	225	2 S37484	Ig kappa chain - m
15	694.5	55.9	218	2 S68241	Ig kappa chain v r
16	688.5	55.4	214	2 S68212	Ig kappa chain (Ma
17	688.5	55.4	218	2 JC5810	monoclonal antibod
18	687.5	55.4	234	2 S14237	Ig kappa chain pre
19	686	55.2	197	2 S29593	Ig kappa chain (WM
20	684.5	55.1	234	2 S01320	Ig kappa chain pre
21	680	54.8	230	2 S31361	Ig kappa chain - s
22	662.5	53.3	210	2 A56169	Ig kappa chain v r
23	644	51.9	235	2 S25058	Ig kappa chain - m
24	617	49.7	178	2 PT0219	Ig kappa chain V-C
25	599	48.2	135	2 S20559	JC-kappa protein -
26	572	46.1	229	2 A20969	Ig kappa chain pre
27	565.5	45.5	140	2 S22658	Ig kappa chain pre
28	552	44.4	133	2 S23230	Ig kappa chain pre
29	552	44.4	133	2 S42611	HUNVK protein prec

30 552 44.4 136 2 S40357 Ig kappa chain V-J
31 550 44.3 133 1 K2HURP Ig kappa chain pre
32 549 44.2 133 2 S40324 Ig kappa chain v r
33 548 44.1 106 1 K3HU Ig kappa chain C r
34 548 44.1 142 2 S22902 Ig kappa chain v r
35 541 43.6 135 2 S40342 Ig kappa chain - h
36 538 43.3 133 1 A24452 Ig kappa chain pre
37 537 43.2 132 2 S26882 Ig kappa chain v r
38 534 43.0 128 2 S40373 Ig kappa chain - h
39 533 42.9 238 2 A49633 Ig lambda-like cha
40 524 42.2 126 2 S40312 Ig kappa chain - h
41 520 41.9 132 2 S40322 Ig kappa chain - h
42 519.5 41.8 131 2 S40355 Ig kappa chain - h
43 513 41.3 99 2 A37927 Ig kappa chain C r
44 510.5 41.1 144 2 PL0106 Ig kappa chain pre
45 508.5 40.9 132 2 PH0106 anti-digoxin trans

ALIGNMENTS

RESULT 1
JE0244
Ig Kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A:Reference number: JE0243
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <Ali>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 915; DB 2; Length 215;

Best Local Similarity 80.9%; Pred.No.1.9e-55;

Matches 178; Conservative 19; Mismatches 17; Indels 6; Gaps 3;

Qy 21 EVYMTQSPLSLPTPEGPASISCRSSQSLKHSNGDTFLSWYQQKFGQPPRLIYKVSNRD 80

Db 1 EVLTQSPATLSVSPGERATLSCRASQSV-HSN---LAWYQQKPGQAPRLIYRASTRA 55

Qy 81 SGVPDRFSGSGAGTDFTLKISAVEADGVGVFCGQGRTPP-TFGSGTKVKIKRTVAAPS 139

Db 56 TGIPTARFSSGSGTDFTLTISLSQSEDFALYYCOQNTWPPLTFGGTKVETIKRTVAAPS 115

Qy 140 VFIPTPSDQLKSGTASVVCLLNNFYPREAKQVQKVDNALQSGNSQESVTEQDSKSDSTYS 199

Db 116 VFIPTPSDQLKSGTASVVCLLNNFYPREAKQVQKVDNALQSGNSQESVTEQDSKSDSTYS 175

Qy 200 LSSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 239

Db 176 LSSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 215

RESULT 2

JE0242

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.

submitted to JIPID, November 1998

A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mult

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <Ali>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-91/Domain: immunoglobulin homology <IMM>

Search completed: April 6, 2003, 06:25:19
Job time : 37.7832 secs



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QY 238 GACTCTGGGTCCAGACAGAGATTTCAGCGCAGTGGGCGAGGACAGATTTCACACTGAAA 297
Db 1254 GAATCTGGGTACCTGACCGATTTCAGTGGCAGCGGTCTGGGACAGATTTCACCTCACC 1313
QY 298 ATCAGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGCGGGCAAGGTACAAAGACT 357
Db 1314 ATCAGCAGCTGCAGGCTGAAGATGTGGCAGTATACACTGTCAAGATGTTCTAGATTTT 1373
QY 358 CTGCCACTTTGGCGGAGGAGCAAGGTGGAATCAAAAGTACGGTGGTGCACCACTCT 417
Db 1374 CCATTACGTTTCGGCGGAGGAGCAAGTTGGAGATCAAAAGTACTGTGGCGGGCCATCT 1433
QY 418 GTCTTTCATCTTCCCGCCATCTGATGACAGTGTGAATCTGGAATCTGGAATCTGTGTGTGC 477
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QY 478 CTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAGGTGGAATCAACGCCCTC 537
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QY 718 TGA 720
Db 1734 TAA 1736
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RESULT 15

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US-08-940-371-50
; Sequence 50, Application US/08940371
; Patent No. 5851525
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P. O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,371
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,110
; FILING DATE:
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; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270-5024
; TELEFAX: 610 270-5090
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5703 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; US-08-940-371-50
Query Match 68.0%; Score 489.4; DB 2; Length 5703;
Best Local Similarity 80.8%; Pred. No. 6.4e-135;
Matches 584; Conservative 0; Mismatches 136; Indels 3; Gaps 1;
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QY 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTCGGTCCCGGGTCCAGTGGG 60
Db 1014 ATGGTGTGCAGACCCAGGTCTTCAATTTCTCTGTGTCTCGATCTCTGGTGCCTACGGG 1073
QY 61 GAAAGTGTGATGACTCAGCTCTCCACTGTCCTTCCATCACACCTGGAGAGCCGCGCTCC 120
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Db 1554 CAATCGGGTAACTCCAGGAGAGTGTCAAGAGCAGGACAGCAAGGACAGCAGCCTACAGC 1613
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Db 1674 GAACTACCCATCAGGCGCTGAGCTCCCGCTCACAAGAGCTTCAACAGGGGAGAGTGT 1733
QY 718 TGA 720
Db 1734 TAA 1736
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; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5703 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-470-110A-50

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Query Match          58.0%; Score 489.4; DB 1; Length 5703;
Best Local Similarity 80.8%; Pred. No. 6.4e-135;
Matches 584; Conservative 0; Mismatches 136; Indels 3; Gaps 1;

QY 1 ATGAGCCTCCCTGCTCAGCTCCTCGGCGCTCTATTGCTCTGCGTCCCGGTCCTCAGTGGG 60
DB 1014 ATGGTGTTCAGACCCAGGCTTCATTTCTGTTGCTCTGGAATCTCTGTGCTCAGGG 1073

QY 61 GAAGTTGTGATGACTCAGTCTCAGTCTCAGTCTGTCCTTCCATCACACCTGAGAGCGGCTCC 120
DB 1074 GATATCGTGATGACCCAGTCTCCAGACTCGTAGCTGTGTCTCTGGGCGAGAGGCCACC 1133

QY 121 ATCTCCGTAGTCTAGTCAAGCGCTTAACACAGT---AATGGACACACTTCTCTGAGT 177
DB 1134 ATCAACTGCAAGAGCTCTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGGCC 1193

QY 178 TGGTATCAGCAGAACCCAGGCCCAACCTCCAAAGGCTCTCTGATTTTATAAGGTTTCTAACCGG 237
DB 1194 TGGTATCAGCAGAACCCAGGCCCAACCTCCAAAGGCTCTCTGATTTTATAAGGTTTCTAACCGG 1253

QY 238 GACTCTGGGTCCGACAGATTCAGCGGCGAGTGGGCGAGGACAGATTTCACATGAAA 297
DB 1254 GAATCTGGGTACCTGACCCGATTCAGTGGCAGCGGCTCGGACAGATTTCACTCTCACC 1313

QY 298 ATCAGCGCAGTGGAGGCTGAAGATGTGGGGTTTATTTCTGCGGCAAGGTACAGGACT 357
DB 1314 ATCAGCGCCTGAGGCTGAAGATGTGGGAGTATCTACTGTCAGAAATGTTTCATAGTTT 1373

QY 358 CCTCCCACTTTCCGCGGAGGACCAAGGTGGAATCAAAAGTACGCTGCGTGGCTGCCACCATCT 417
DB 1374 CCATTACGTTTCGCGGAGGACCAAGTTGGAGATCAAAAGTACTGTGGCGGCGCATCT 1433

QY 418 GTCTTCATCTCCGCGCATCTGATGAGCAGTGTGAATCTGGAATCTGCTGTTGTGTGC 477
DB 1434 GTCTTCATCTCCGCGCATCTGATGAGCAGTGTGAATCTGGAATCTGCTGTTGTGTGC 1493

QY 478 CTGCTGAATAACTTCTATCCAGAGAGGCAAAAGTACAGTGAAGGTGATACGCGCTC 537
DB 1494 CTGCTGAATAACTTCTATCCAGAGAGGCAAAAGTACAGTGAAGGTGATACGCGCTC 1553

QY 538 CAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACACACCTACAGC 597
DB 1554 CAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACACACCTACAGC 1613

QY 598 CTCAGCAGCAGCCTGAGCTGAGCAAGCAGACTACAGAGAAACACAAAGTCTACGCGCTC 657
DB 1614 CTCAGCAGCAGCCTGAGCTGAGCAAGCAGACTACAGAGAAACACAAAGTCTACGCGCTC 1673

QY 658 GAAGTCAACCATCAGGCGCTGAGCTGCCCGTTCACAAAGAGCTTCAACAGGGGAGAGTGT 717
DB 1674 GAAGTCAACCATCAGGCGCTGAGCTGCCCGTTCACAAAGAGCTTCAACAGGGGAGAGTGT 1733

QY 718 TGA 720
DB 1734 TAA 1736
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RESULT 14
US-08-667-769A-50
; Sequence 50, Application US/08667769A
; Patent No. 5783184
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.

```
; APPLICANT: Chaiken, Irwin M.  
; APPLICANT: Cook, Richard M.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: McMillan, Lynette J.  
; APPLICANT: Theisen, Timothy W.  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; STREET: P.O. Box 1539-UW2220  
; CITY: King of Prussia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/667,769A  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/17082  
; FILING DATE: 22-DEC-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/470110  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/467420  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/363131  
; FILING DATE: 23-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50503  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5024  
; TELEFAX: 610-270-5090  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5703 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
US-08-667-769A-50
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Query Match          68.0%; Score 489.4; DB 1; Length 5703;
Best Local Similarity 80.8%; Pred. No. 6.4e-135;
Matches 584; Conservative 0; Mismatches 136; Indels 3; Gaps 1;

QY 1 ATGAGCCTCCCTGCTCAGCTCCTCGGCGCTCTATTGCTCTGCGTCCCGGTCCTCAGTGGG 60
DB 1014 ATGGTGTTCAGACCCAGGCTTCATTTCTGTTGCTCTGGAATCTCTGTGCTCAGGG 1073

QY 61 GAAGTTGTGATGACTCAGTCTCAGTCTCAGTCTGTCCTTCCATCACACCTGAGAGCGGCTCC 120
DB 1074 GATATCGTGATGACCCAGTCTCCAGACTCGTAGCTGTGTCTCTGGGCGAGAGGCCACC 1133

QY 121 ATCTCCGTAGTCTAGTCAAGCGCTTAAACACAGT---AATGGACACACTTCTCTGAGT 177
DB 1134 ATCAACTGCAAGAGCTCTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGGCC 1193

QY 178 TGGTATCAGCAGAACCCAGGCCCAACCTCCAGGCTCTCTGATTTTATAAGGTTTCTAACCGG 237
DB 1194 TGGTATCAGCAGAACCCAGGCCCAACCTCCAGGCTCTCTGATTTTATAAGGTTTCTAACCGG 1253
```

APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P. O. Box 1539-UM2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,420A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 5703 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-467-420A-50

Query Match 68.0%; Score 489,4; DB 1; Length 5703;
Best Local Similarity 80.8%; Pred. No. 6,4e-135;
Matches 584; Conservative 0; Mismatches 136; Indels 3; Gaps 1;
QY 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGGCTCCCGGGTCCAGTGGG 60
DB 1014 ATGGTGTTCAGACCCAGGCTTCATTCTCTGCTCTGGATCTCTGGTGCCTACGGG 1073
QY 61 GAAGTTGTGATGACTAGTCTCAGCTGCTCCCTCCATCACACTCGAGAGCGGGCTCC 120
DB 1074 GATATCGTGTGATGACCCAGTCTCCAGACTCGCTAGCTGTGCTCTGGCGGAGAGGGCCACC 1133
QY 121 ATCTCTGTAGTCTAGCTCAAGCTTAAACACAGT---AATGGACACCTTCCTGAGT 177
DB 1134 ATCACTGCAAGACTCTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTTGGCC 1193
QY 178 TGGTATCAGCAGAGGCGAGGCCAACCTCCAGGCTCTCTGATTTTAAAGTTTCTAACCGG 237
DB 1194 TGGTATCAGCAGAAACCCGGGAGCTCTCTAAAGTTGCTATTTACGGGGCTCGACTAG 1253
QY 238 GACTCTGGGTCCAGACAGATTTCAGCGGAGTGGGCGAGGACAGATTCACACTGAA 297
DB 1254 GAATCTGGGGTACCTGACCGATTTCAGTGGCAGCGGGTCTGGGACAGATTCCTCACC 1313
QY 298 ATCAGCGCAGTGGAGGCTGAAGATGTTGGGTTTATTTCTGCGGGCAAGGTACAAGACT 357
DB 1314 ATCAGCAGCCTGCAGGCTGAAGATGTCGAGTATCTACTGTCTAGATGTTTCATAGTTT 1373

QY 358 CCTCCCACTTTCCGCGGAGGACCAAGGTGGAATCAAAAGTACGGTGGCTGCACCATCT 417
DB 1374 CCAATTCAGTTCCGCGGAGGACCAAGTTGGAGATCAAAAGTACTGTGGCGGCGCATCT 1433
QY 418 GTCTTCATCTTCCGCGCATCTGATGAGCAGTTGAAATCTGAAATCTGCTCTGTGTGTGC 477
DB 1434 GTCTTCATCTTCCGCGCATCTGATGAGCAGTTGAAATCTGAAATCTGCTCTGTGTGTGC 1493
QY 478 CTGCTGAATAACTTTCTATCCAGAGAGGCCAAAGTACAGTGGAGTGGATAACGCCCTC 537
DB 1494 CTGCTGAATAACTTTCTATCCAGAGAGGCCAAAGTACAGTGGAGTGGATAACGCCCTC 1553
QY 538 CAATCGGGTAACTCCAGAGAGTGTACAGAGCAGGACAGCAGGACAGCAGCTACAGC 597
DB 1554 CAATCGGGTAACTCCAGAGAGTGTACAGAGCAGGACAGCAGGACAGCAGCTACAGC 1613
QY 598 CTCAGCAGCAGCCTGAGCTGAGCAAAAGCAGACTTACAGAGAAACACAAGTCTACGCCCTGC 657
DB 1614 CTCAGCAGCAGCCTGAGCTGAGCAAAAGCAGACTTACAGAGAAACACAAGTCTACGCCCTGC 1673
QY 658 GAAGTCAACCATCAGGCGCTGAGCTCGCCCTCACAAGAGCTTCAACAGGGGAGAGTGT 717
DB 1674 GAAGTCAACCATCAGGCGCTGAGCTCGCCCTCACAAGAGCTTCAACAGGGGAGAGTGT 1733
QY 718 TGA 720
DB 1734 TAA 1736

RESULT 13

US-08-470-110A-50
Sequence 50, Application US/08470110A
Patent No. 5693323
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P. O. Box 1539-UM2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,110A
FILING DATE:
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5090

APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
NUMBER OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
US-09-026-985-41

Query Match 72.1%; Score 519.2; DB 3; Length 729;
Best Local Similarity 86.7%; Pred. No. 4.4e-144;
Matches 572; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCTCCATCACACCTGGAGAGCGGCTCC 120
DB 70 GATATCGTATGACACAGACCACTCTCCCTGCTGTCAGTCTTGGAGATCAGGCTCC 129

QY 121 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAAATGAGACACCTTCTGAGTTGG 180
DB 130 AICTCTTGCAGATCTAGTACAGCCTTGTACCGTATTGGAACACCTATTACATTGG 189

QY 181 TATCAGCAGAAGCCAGGCCAACTCCAAAGCTCTCTGATTATAAGTTTCTAAACCGGAC 240
DB 190 TACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAAACCGATT 249

QY 241 TCTGGGCTCCAGACAGATTACGGGCTGAGGAGGAGGACAGATTTCACACTGAAATC 300
DB 250 TCTGGGCTCCAGACAGATTACGGGCTGAGGAGGAGGACAGATTTCACACTGAGGATC 309

QY 301 AGCCAGTGGAGGCTGAAGATGTTGGGGTTATTTCTGGGGCAAGGTACAAAGACTCTCT 360
DB 310 AGCAGAGTGGAGGCTGAGGATCTGGGACTTTATTTCTGCTCTCAAGATACACATGTCG 369

QY 361 CCACATTTCCGCGGAGGACCAAGTGGAAATCAACGTTACGTTGCTGCTGACATCTGTC 420
DB 370 CTCACGTTCCGCTGCTGGGACCAAGCTGGAGCTGAAACGGGCTGTTGCTGACCAACTGA 429

QY 421 TTCACTCTCCGCGCATCTGATGAGCAGTTGAAATCTGGAACTGCTCTGTTGTGTCCTG 480
DB 430 TTCACTCTCCGCGCATCTGATGAGCAGTTGAAATCTGGAACTGCTCTGTTGTGTCCTG 489

QY 481 CTGAATTAATCTTATCCAGAGAGGCAAGTACAGTGAAGTGGATACCCCTTCCAA 540
DB 490 CTGAATTAATCTTATCCAGAGAGGCAAGTACAGTGAAGTGGATACCCCTTCCAA 549

QY 541 TCGGTTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACTTACAGCCTC 600

DB 550 TCGGTAACTCCGAGGAGAGTGTCTACAGAGAGGACACAAAGGACAGCACTTACAGCCTC 609
QY 601 AGCAGCACCTCTGACCTGAGCAAGCAGACTACGAGAAACACAAAGTCTAGCCTTGCAGAA 660
DB 610 AGCAGCACCTCTGACCTGAGCAAGCAGACTACGAGAAACACAAAGTCTAGCCTTGCAGAA 669
QY 661 GTACCCATCAGGCTGAGCTGCGCCCTTCAAAAGAGCTTCAACAGGGGAGAGTTGA 720
DB 670 GTACCCATCAGGCTGAGCTGCGCCCTTCAAAAGAGCTTCAACAGGGGAGAGTTGA 729

RESULT 10

US-09-121-952A-41
Sequence 41, Application US/09121952A
Patent No. 6458355
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-Jul-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
US-09-121-952A-41

Query Match 72.1%; Score 519.2; DB 4; Length 729;
Best Local Similarity 86.7%; Pred. No. 4.4e-144;
Matches 572; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCTCCATCACACCTGGAGAGCGGCTCC 120
DB 70 GATATCGTATGACACAGACCACTCTCCCTGCTGTCAGTCTTGGAGATCAGGCTCC 129

QY 121 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAAATGAGACACCTTCTGAGTTGG 180
DB 130 ATCTCTGTAGTCTAGTCAAGCCTTGTACAGGCTTGTACAGGTAATGGAACACCTATTACATTGG 189

Query Match 72.1%; Score 519.2; DB 3; Length 729;
Best Local Similarity 86.7%; Pred. No. 4.4e-144;
Matches 572; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCTTCCCATCACACCTGGAGAGCGGCTCC 120
DB 70 GATATCGTGATGACACAGACCACTCTCCCTGCTGTGAGATCAGGCTCC 129

QY 121 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAATGGAGACACCTTCTGAGTTGG 180
DB 130 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAATGGAGACACCTTCTGAGTTGG 189

QY 181 TATCAGCAGAGCGGCTGAGTCTCCAGGCTCTCTGATTTATTAAGGTTTCTAACCGGAC 240
DB 190 TACCTGCAGAAAGCGGCTGAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATT 249

QY 241 TCTGGGTTCCAGACAGATTTCAGGGCAGTGGGCGAGGACAGATTTTCACACTGAAATC 300
DB 250 TCTGGGTTCCAGACAGATTTCAGGGCAGTGGGCGAGGACAGATTTTCACACTGAAATC 309

QY 301 AGGCGAGTGGAGCTGAGTCTGGGTTTATTTCTGGGCGAGGACAGTCTGAGGACTCCT 360
DB 310 AGCAGAGTGGAGCTGAGTCTGGGTTTATTTCTGCTCTCAAGTACACATGTTCCG 369

QY 361 CCCACTTTCGGGCGAGGACCAAGGTGGAATCAACGCTACGCTGGCTGCACCATCTGTC 420
DB 370 CTCAGGTTGGTGCTGGGACCAAGCTGGAGCTGAAACGGGCTGTTGCTGCACCACTGTA 429

QY 421 TTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATCTGCCCTCTGTTGTGCTG 480
DB 430 TTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATCTGCCCTCTGTTGTGCTG 489

QY 481 CTGAATAACTTCTATCCAGAGAGTGTACAGAGCAGGACAGCAAGCAGACCTACAGCCTC 540
DB 490 CTGAATAACTTCTATCCAGAGAGTGTACAGAGCAGGACAGCAAGCAGACCTACAGCCTC 549

QY 541 TCGGGTAACTCCAGAGAGTGTACAGAGCAGGACAGCAAGGACAGCAAGCTTACGCTCGCAA 600
DB 550 TCGGGTAACTCCAGAGAGTGTACAGAGCAGGACAGCAAGGACAGCAAGCTTACGCTCGCAA 609

QY 601 AGCAGCAGCTGAGCCTGAGCAAGAGCAGCTACGAGAAACACAAAGTCTACGCTCGCAA 660
DB 610 AGCAGCAGCTGAGCCTGAGCAAGAGCAGCTACGAGAAACACAAAGTCTACGCTCGCAA 669

QY 661 GTCAACCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGAGGTGTTAA 720
DB 670 GTCAACCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGAGGTGTTAA 729

RESULT 8
US-08-804-444A-41
; Sequence 41, Application US/08804444A
; Patent No. 6117980
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania N
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,444A

FILING DATE: 21-Feb-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
US-08-804-444A-41

Query Match 72.1%; Score 519.2; DB 3; Length 729;
Best Local Similarity 86.7%; Pred. No. 4.4e-144;
Matches 572; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCTTCCCATCACACCTGGAGAGCGGCTCC 120
DB 70 GATATCGTGATGACACAGACCACTCTCCCTGCTGTGAGATCAGGCTCC 129

QY 121 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAATGGAGACACCTTCTGAGTTGG 180
DB 130 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAATGGAGACACCTTCTGAGTTGG 189

QY 181 TATCAGCAGAGCGGCTGAGTCTCCAGGCTCTCTGATTTATTAAGGTTTCTAACCGGAC 240
DB 190 TACCTGCAGAAAGCGGCTGAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATT 249

QY 241 TCTGGGTTCCAGACAGATTTCAGGGCAGTGGGCGAGGACAGATTTTCACACTGAAATC 300
DB 250 TCTGGGTTCCAGACAGATTTCAGGGCAGTGGGCGAGGACAGATTTTCACACTGAAATC 309

QY 301 AGGCGAGTGGAGCTGAGTCTGGGTTTATTTCTGGGCGAGGACAGTCTGAGGACTCCT 360
DB 310 AGCAGAGTGGAGCTGAGTCTGGGTTTATTTCTGCTCTCAAGTACACATGTTCCG 369

QY 361 CCCACTTTCGGGCGAGGACCAAGGTGGAATCAACGCTACGCTGGCTGCACCATCTGTC 420
DB 370 CTCAGGTTGGTGCTGGGACCAAGCTGGAGCTGAAACGGGCTGTTGCTGCACCACTGTA 429

QY 421 TTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATCTGCCCTCTGTTGTGCTG 480
DB 430 TTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATCTGCCCTCTGTTGTGCTG 489

QY 481 CTGAATAACTTCTATCCAGAGAGTGTACAGAGCAGGACAGCAAGGACAGCAAGCTTACGCTCGCAA 540
DB 490 CTGAATAACTTCTATCCAGAGAGTGTACAGAGCAGGACAGCAAGGACAGCAAGCTTACGCTCGCAA 549

QY 541 TCGGGTAACTCCAGAGAGTGTACAGAGCAGGACAGCAAGGACAGCAAGCTTACGCTCGCAA 600
DB 550 TCGGGTAACTCCAGAGAGTGTACAGAGCAGGACAGCAAGGACAGCAAGCTTACGCTCGCAA 609

QY 601 AGCAGCAGCTGAGCCTGAGCAAGAGCAGCTACGAGAAACACAAAGTCTACGCTCGCAA 660
DB 610 AGCAGCAGCTGAGCCTGAGCAAGAGCAGCTACGAGAAACACAAAGTCTACGCTCGCAA 669

QY 661 GTCAACCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGAGGTGTTAA 720
DB 670 GTCAACCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGAGGTGTTAA 729

RESULT 9
US-09-026-985-41
; Sequence 41, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.

Qy	361	CCCATCTTCGGCGGAGGGA	CCAAAGGTGAAATCAAA	CGTACGGTGGCTGCACCATCTGTG	420
Db	370	CTCAGCTTCGGTGTCTGG	ACCAAGCTGGAGCTGAA	ACGGCTCTGCTGCACCACTGTA	429
Qy	421	TTCAATCTCCCGGCATCT	GAATGAGCAGTTCGAA	ATCTGGAACTCCCTCTCTGTGTGCTG	480
Db	430	TTCAATCTCCCAACCAT	CCAGTGAAGCAATTCG	AAATCTGGAACTCCCTCTCTGTGTGCTG	489
Qy	481	CTGAATAACTTCTATCC	AGAGAGGCCAAAGTACA	GTGAGTGGNAGTGGATTAACGCGCTCCAA	540
Db	490	CTGAATAACTTCTATCC	AGAGAGGCCAAAGTACA	GTGAGTGGNAGTGGATTAACGCGCTCCAA	549
Qy	541	TCGGGTAACTCCAGGAG	AGTGTCTACAGAGCAG	CAGCAGCAAGAGCAGCAGCTACAGCCTC	600
Db	550	TCGGGTAACTCCAGGAG	AGTGTCTACAGAGCAG	CAGCAGCAAGAGCAGCAGCTACAGCCTC	609
Qy	601	AGCAGCACTCTGACGCT	GTGACCAAGCAGACTT	ACGAGAAAACAAAAGTCTACGCGCTCGAA	660
Db	610	AGCAGCACTCTGACGCT	GTGACCAAGCAGACTT	ACGAGAAAACAAAAGTCTACGCGCTCGAA	669
Qy	661	GTACCCCATCAGGCGCT	TGAGCTCGCCCGTCA	CAAAAGAGCTTCAACAGGCGAGAGTGTGA	720
Db	670	GTACCCCATCAGGCGCT	TGAGCTCGCCCGTCA	CAAAAGAGCTTCAACAGGCGAGAGTGTGA	729
RESULT 7					
US-09-027-449-41					
: Sequence 41, Application US/09027449					
: Patent No. 6025158					
: GENERAL INFORMATION:					
: APPLICANT: Gonzalez, Tania R.					
: APPLICANT: Leong, Steven R.					
: APPLICANT: Presta, Leonard G.					
: TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and					
: TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies					
: NUMBER OF SEQUENCES: 72					
: CORRESPONDENCE ADDRESS:					
: ADDRESSEE: Genentech, Inc.					
: STREET: 1 DNA Way					
: CITY: South San Francisco					
: STATE: California					
: COUNTRY: USA					
: ZIP: 94080					
: COMPUTER READABLE FORM:					
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk					
: COMPUTER: IBM PC compatible					
: OPERATING SYSTEM: PC-DOS/MS-DOS					
: SOFTWARE: WinFatin (Genentech)					
: CURRENT APPLICATION DATA:					
: APPLICATION NUMBER: US/09/027,449					
: FILING DATE: 20-Feb-1998					
: CLASSIFICATION: 435					
: PRIOR APPLICATION DATA:					
: APPLICATION NUMBER: 60/074,330					
: FILING DATE: 22-Jan-1998					
: PRIOR APPLICATION DATA:					
: APPLICATION NUMBER: 60/038,664					
: FILING DATE: 21-Feb-1997					
: ATTORNEY/AGENT INFORMATION:					
: NAME: Love, Richard B.					
: REGISTRATION NUMBER: 34,659					
: REFERENCE/DOCKET NUMBER: P1085R3-2					
: TELECOMMUNICATION INFORMATION:					
: TELEPHONE: 650/225-5530					
: TELEFAX: 650/952-9881					
: INFORMATION FOR SEQ ID NO: 41:					
: SEQUENCE CHARACTERISTICS:					
: LENGTH: 729 base pairs					
: TYPE: Nucleic Acid					
: STRANDEDNESS: Double					
: TOPOLOGY: Linear					
: US-09-027-449-41					

US-08-396-851A-55

Query Match 72.1%; Score 519.2; DB 1; Length 729;
Best Local Similarity 86.7%; Pred. No. 4.4e-144;
Matches 572; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCTCCATCCATCCAGAGCGGCTCC 120
DB 70 GATATCGTGTGATGACACAGACACACTCTCCCTGCTGCTGATGATGAGGCTCC 129

QY 121 ATCTCTGTAGTCTAGTCAAGCCCTTAAACACAGTAATGAGACACCTTCTCTGAGTTGG 180
DB 130 ATCTCTGTGAGTCTAGTCAAGCCCTTAAACACAGTAATGAGACACCTTCTCTGAGTTGG 189

QY 181 TATCAGCAGAGGAGCGGCAACCTCCAGGCTCTCTGATTTATATAGTTTCTTACCGGGAC 240
DB 190 TACCTGAGAGGAGCGGCAACCTCCAGGCTCTCTGATTTATATAGTTTCTTACCGGGAC 249

QY 241 TCTGGGGTCCAGACAGATTCAGCGGAGTGGGGAGGAGACAGATTTCACATGAAATC 300
DB 250 TCTGGGGTCCAGACAGATTCAGCGGAGTGGGGAGGAGACAGATTTCACATGAAATC 309

QY 301 AGCGCAGTGTGAGGCTGAGATGCTGGGGTTTATTTCTGCGGGCAAGGTCAAGGACTCT 360
DB 310 AGCAGAGTGTGAGGCTGAGATGCTGGGGTTTATTTCTGCGGGCAAGGTCAAGGACTCT 369

QY 361 CCACATTTCCCGGCTGATGAGCAGTGTGAATCTGGAAGCTGCTGTTGTGCTGCTG 420
DB 421 TCCATCTTCCCGGCTGATGAGCAGTGTGAATCTGGAAGCTGCTGTTGTGCTGCTG 429

QY 481 CTGNATTAATCTTATCCAGAGAGGCGCAAGTACAGTGGAGTGGATACAGCCCTCCAA 540
DB 490 CTGAATAATCTTATCCAGAGAGGCGCAAGTACAGTGGAGTGGATACAGCCCTCCAA 549

QY 541 TCGGGTAATCTCCAGGAGAGTGTACAGAGCAGGACAGCAGCAGCAGCAGCAGCCTC 600
DB 550 TCGGGTAATCTCCAGGAGAGTGTACAGAGCAGGAGCAGCAGCAGCAGCAGCCTC 609

QY 601 AGCAGACCTGAGCTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
DB 610 AGCAGACCTGAGCTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 669

QY 661 GTACCCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTGA 720
DB 670 GTACCCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTGA 729

RESULT 5

US-08-396-851A-55
; Sequence 55, Application US/08396851A
; Patent No. 5707622
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,851A
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 874P1-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1489
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-396-851A-55

Query Match 72.1%; Score 519.2; DB 1; Length 729;
Best Local Similarity 86.7%; Pred. No. 4.4e-144;
Matches 572; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCTCCATCCATCCAGAGCGGCTCC 120
DB 70 GATATCGTGTGATGACACAGACACACTCTCCCTGCTGCTGATGATGAGGCTCC 129

QY 121 ATCTCTGTAGTCTAGTCAAGCCCTTAAACACAGTAATGAGACACCTTCTCTGAGTTGG 180
DB 130 ATCTCTGTGAGTCTAGTCAAGCCCTTAAACACAGTAATGAGACACCTTCTCTGAGTTGG 189

QY 181 TATCAGCAGAGGAGCGGCAACCTCCAGGCTCTCTGATTTATATAGTTTCTTACCGGGAC 240
DB 190 TACCTGAGAGGAGCGGCAACCTCCAGGCTCTCTGATTTATATAGTTTCTTACCGGGAC 249

QY 241 TCTGGGGTCCAGACAGATTCAGCGGAGTGGGGAGGAGACAGATTTCACATGAAATC 300
DB 250 TCTGGGGTCCAGACAGATTCAGCGGAGTGGGGAGGAGACAGATTTCACATGAAATC 309

QY 301 AGCGCAGTGTGAGGCTGAGATGCTGGGGTTTATTTCTGCGGGCAAGGTCAAGGACTCT 360
DB 310 AGCAGAGTGTGAGGCTGAGATGCTGGGGTTTATTTCTGCGGGCAAGGTCAAGGACTCT 369

QY 361 CCACATTTCCCGGCTGATGAGCAGTGTGAATCTGGAAGCTGCTGTTGTGCTGCTG 420
DB 370 TCCATCTTCCCGGCTGATGAGCAGTGTGAATCTGGAAGCTGCTGTTGTGCTGCTG 429

QY 421 TCCATCTTCCCGGCTGATGAGCAGTGTGAATCTGGAAGCTGCTGTTGTGCTGCTG 480
DB 430 TCCATCTTCCCGGCTGATGAGCAGTGTGAATCTGGAAGCTGCTGTTGTGCTGCTG 489

QY 481 CTGAATAATCTTATCCAGAGAGGCGCAAGTACAGTGGAGTGGATACAGCCCTCCAA 540
DB 490 CTGAATAATCTTATCCAGAGAGGCGCAAGTACAGTGGAGTGGATACAGCCCTCCAA 549

QY 541 TCGGGTAATCTCCAGGAGAGTGTACAGAGCAGGACAGCAGCAGCAGCAGCAGCCTC 600
DB 550 TCGGGTAATCTCCAGGAGAGTGTACAGAGCAGGAGCAGCAGCAGCAGCAGCCTC 609

QY 601 AGCAGACCTGAGCTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
DB 610 AGCAGACCTGAGCTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 669

QY 661 GTACCCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTGA 720
DB 670 GTACCCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTGA 729

Best Local Similarity 100.0%; Pred. No. 2e-203; 0; Gaps 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0;

Qy 1 ATGAGCCTCCCTGCTCAGCTCCTCGGCTCTATTGCTCTGCTCCCGGGTCCAGTGGG 60
Db 1 ATGAGCCTCCCTGCTCAGCTCCTCGGCTCTATTGCTCTGCTCCCGGGTCCAGTGGG 60

Qy 61 GAAGTTGTGATGACTCAGTCTCAGCTGTCCCTTCCCATCACACCTGGAGAGCGGCTCC 120
Db 61 GAAGTTGTGATGACTCAGTCTCAGCTGTCCCTTCCCATCACACCTGGAGAGCGGCTCC 120

Qy 121 ATCTCTGTAGTCTAGTCTCAAGCTTAAACACAGTAATGGAGACACCTTCTTGAGTTGG 180
Db 121 ATCTCTGTAGTCTAGTCTCAAGCTTAAACACAGTAATGGAGACACCTTCTTGAGTTGG 180

Qy 181 TATCAGCAGAACCCAGCCCACTTCAAGCTCTCTGATTTAATAGTTTCTAACCGGGAC 240
Db 181 TATCAGCAGAACCCAGCCCACTTCAAGCTCTCTGATTTAATAGTTTCTAACCGGGAC 240

Qy 241 TCTGGGGTCCAGACAGATTCAGCGGCTGAGGAGGAGGACAGATTTACACCTGAAATC 300
Db 241 TCTGGGGTCCAGACAGATTCAGCGGCTGAGGAGGAGGACAGATTTACACCTGAAATC 300

Qy 301 AGCCAGTGGAGGCTGAAGTGTGGGGTTTATTTCTGCGGGCAAGGTACAAGGACTCCT 360
Db 301 AGCCAGTGGAGGCTGAAGTGTGGGGTTTATTTCTGCGGGCAAGGTACAAGGACTCCT 360

Qy 361 CCCACTTTCCGCGGAGGAGGACAGAGTGGAAATCAAACTGAGTGGCTGACCATCTGTC 420
Db 361 CCCACTTTCCGCGGAGGAGGACAGAGTGGAAATCAAACTGAGTGGCTGACCATCTGTC 420

Qy 421 TTCACTTTCCGCGCATCTGATGAGCAGTGTAAATCTGGAATCTGCTCTGTGTGGCTG 480
Db 421 TTCACTTTCCGCGCATCTGATGAGCAGTGTAAATCTGGAATCTGCTCTGTGTGGCTG 480

Qy 481 CTGAATTAATCTTATCCAGAGAGGCAAGTACAGTGAAGTGTGAATACCGCTCCAA 540
Db 481 CTGAATTAATCTTATCCAGAGAGGCAAGTACAGTGAAGTGTGAATACCGCTCCAA 540

Qy 541 TCGGGTAACTCCAGAGAGTGTACAGAGCAGGACAGCAAGGACAGACCTTACAGCCTC 600
Db 541 TCGGGTAACTCCAGAGAGTGTACAGAGCAGGACAGCAAGGACAGACCTTACAGCCTC 600

Qy 601 AGCAGCCTTACGCTGAGCAAGAGCAGTACAGAAACACAAAGTCTACCGCTCCGAA 660
Db 601 AGCAGCCTTACGCTGAGCAAGAGCAGTACAGAAACACAAAGTCTACCGCTCCGAA 660

Qy 661 GTCAACCATCAGGCGCTGAGTCCCGTCCAAAGAGCTTCAACAGGGGAGAGTGTGA 720
Db 661 GTCAACCATCAGGCGCTGAGTCCCGTCCAAAGAGCTTCAACAGGGGAGAGTGTGA 720

RESULT 2

US-08-398-613A-55
; Sequence 55, Application US/08398613A
; Patent No. 5677426
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,613A
FILING DATE: 01-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 874P1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1489
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-398-613A-55

Query Match 72.1%; Score 519.2; DB 1; Length 729;

Best Local Similarity 86.7%; Pred. No. 4.4e-144; Indels 0; Gaps 0;

Matches 572; Conservative 0; Mismatches 88;

Qy 61 GAAGTTGTGATGACTCAGTCTCAGCTGTCCCTTCCCATCACACCTGGAGAGCGGCTCC 120
Db 70 GATATCGTATGACACAGACACCACTCTCCCTGCTGTCAGTCTTGGAGATCAGGCTCC 129

Qy 121 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAATGGAGACACCTTCTTGAGTTGG 180
Db 130 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAATGGAGACACCTTCTTGAGTTGG 189

Qy 181 TATCAGCAGAACCCAGCCCACTTCAAGCTCTCTGATTTAATAGTTTCTAACCGGGAC 240
Db 190 TACCTCGAGAGCCAGGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACGATTT 249

Qy 241 TCTGGGGTCCAGACAGATTCAGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
Db 250 TCTGGGGTCCAGACAGATTCAGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 309

Qy 301 AGCGCAGTGGAGGCTCAAGATGTGGGGTTTATTTCTGCGGCAAGGTACAAGGACTCCT 360
Db 310 AGCAGAGTGGAGGCTGAGGATCTGGGACTTTTATTTCTGCTCTCAAAGTACACATGTTCCG 369

Qy 361 CCACCTTTCCGCGGAGGAGGACCAAGGTGGAAATCAAACTGACGTTGCGCTGCAACCTCTCTC 420
Db 370 CTCACGTTCCGCTGCGGACCAAGCTGGAGCTGAAACCGGGCTGTTGCTGCAACCACTGTA 429

Qy 421 TTCACTTTCCCGCATCTGATGAGCAGTGTAAATCTGGAATCTGGAATCTGTTGTGTCCTG 480
Db 430 TTCACTTTCCCGCATCTGATGAGCAGTGTAAATCTGGAATCTGGAATCTGTTGTGTCCTG 489

Qy 481 CTGAATAAATCTTCTATCCAGAGAGGCGCAAGGTACAGTGGAAAGTGAATAGCCCTCCAA 540
Db 490 CTGAATAAATCTTCTATCCAGAGAGGCGCAAGGTACAGTGGAAAGTGAATAGCCCTCCAA 549

Qy 541 TCGGGTAACTCCAGAGAGTGTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
Db 550 TCGGGTAACTCCAGAGAGTGTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 609

Qy 601 AGCAGCAGCCTTACGCTGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 610 AGCAGCAGCCTTACGCTGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 669

Qy 661 GTCAACCATCAGGCGCTGAGTCCCGCTCAAAAGAGCTTCAAAAGAGGAGGAGGAGGAGGAGGAGG 720
Db 670 GTCAACCATCAGGCGCTGAGTCCCGCTCAAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 729

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:47:34 ; Search time 32.7832 Seconds
(without alignments)
6735.375 Million cell updates/sec

Title: US-09-758-173-5

Perfect score: 720

Sequence: 1 ATGAGCTCCTGCTGAGCT.....TCACAGGGGAGAGTGTGA 720

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	720	100.0	720	3	US-08-487-550-5
2	519.2	72.1	729	1	US-08-398-613A-55
3	519.2	72.1	729	1	US-08-398-612A-55
4	519.2	72.1	729	1	US-08-398-611A-55
5	519.2	72.1	729	1	US-08-396-851A-55
6	519.2	72.1	729	2	US-08-491-334A-55
7	519.2	72.1	729	3	US-09-027-449-41
8	519.2	72.1	729	3	US-08-804-444A-41
9	519.2	72.1	729	3	US-09-026-985-41
10	519.2	72.1	729	4	US-09-121-952A-41
11	519.2	72.1	729	4	US-09-234-340A-41
12	489.4	68.0	5703	1	US-08-467-420A-50
13	489.4	68.0	5703	1	US-08-470-110A-50
14	489.4	68.0	5703	1	US-08-667-769A-50
15	489.4	68.0	5703	2	US-08-940-371-50
16	489.4	68.0	5703	3	US-08-637-647-50
17	489.4	68.0	5703	5	PCT-US95-17082A-50
18	486.4	67.6	19040	4	US-09-343-485A-3
19	474.8	65.9	931	3	US-09-049-672A-19
20	471.6	65.5	1066	1	US-08-157-101A-4
21	468.8	65.1	705	1	US-08-488-376-16
22	468.8	65.1	705	2	US-08-634-223-16
23	468.8	65.1	705	2	US-08-634-224-16
24	468.8	65.1	705	2	US-08-634-400-16
25	468.8	65.1	705	2	US-08-635-878-16
26	468.8	65.1	705	2	US-08-770-057-16
27	468.8	65.1	705	4	US-09-335-697B-16

28 468.8 65.1 705 4 US-09-335-697B-16 Sequence 16, Appl
29 462 64.2 729 1 US-08-276-852-152 Sequence 152, App
30 462 64.2 729 1 US-08-276-852-152 Sequence 152, App
31 462 64.2 729 1 US-08-899-575-152 Sequence 152, App
32 462 64.2 729 1 US-08-899-575-152 Sequence 152, App
33 462 64.2 729 1 US-08-899-575-152 Sequence 152, App
34 462 64.2 729 1 US-08-899-575-152 Sequence 152, App
35 462 64.2 729 5 PCT-US95-08743-152 Sequence 168, App
36 462 64.2 729 5 PCT-US95-08743-152 Sequence 152, App
37 462 64.2 729 5 PCT-US95-08743-152 Sequence 152, App
38 462 64.2 729 5 PCT-US95-08743-152 Sequence 152, App
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42 462 64.2 729 5 PCT-US95-08743-152 Sequence 152, App
43 462 64.2 729 5 PCT-US95-08743-152 Sequence 152, App
44 462 64.2 729 5 PCT-US95-08743-152 Sequence 152, App
45 460.4 63.9 3819 4 US-09-042-353-393 Sequence 393, App

ALIGNMENTS

RESULT 1
US-08-487-550-5
; Sequence 5, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 720 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..720
; NAME/KEY: mat_peptide
; LOCATION: 1..720
US-08-487-550-5
Query Match 100.0%; Score 720; DB 3; Length 720;

us-09-758-173-7.rge

Sun Apr 6 09:17:24 2003

Db 1401 GAGGCTCTGCACAAACCACTACACGACAGAGGCTCTCCCTGTCTCCGGGTAAATGA 1457

Search completed: April 6, 2003, 01:56:13
Job time : 4520.08 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:13:05 ; Search time 4509.08 Seconds
(without alignments)
9274.790 Million cell updates/sec

Title: US-09-758-173-7

Perfect score: 1437

Sequence: 1 ATGGGTGGAGCCTCATCTT.....CCCTGCTCCGGTAAATGA 1437

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vt.*

14: gb_vt.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_mu.*

21: em_mu.*

22: em_mu.*

23: em_mu.*

24: em_mu.*

25: em_mu.*

26: em_mu.*

27: em_mu.*

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29: em_mu.*

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32: em_mu.*

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40: em_mu.*

41: em_mu.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1437	100.0	1437	6	AR108865	Sequence
2	1238.6	86.2	1642	9	AK093806	Homo sapi
3	1219	84.8	7521	6	AX080951	Sequence
4	1208	84.1	1659	9	BC014667	Homo sapi
5	1189.2	82.8	1666	9	BC006402	Homo sapi
6	1188.2	82.7	1679	9	BC018747	Homo sapi
7	1186.2	82.5	1630	9	BC024289	Homo sapi
8	1185	82.5	1430	6	AX419496	Sequence
9	1184.6	82.4	1549	6	A21385	plasmid DNA
10	1184	82.4	1673	9	HSIGG1LH	Homo sapien
11	1183.4	82.4	1633	9	AK097859	Homo sapi
12	1182.2	82.3	1990	9	AK098817	Homo sapi
13	1173	81.6	1631	9	AK097010	Homo sapi
14	1171.8	81.5	3143	9	BC019046	Homo sapi
15	1169.4	81.4	1624	9	HSIGG1KH	Homo sapien
16	1166.6	81.2	1633	9	AK097367	Homo sapi
17	1162.2	80.9	1419	12	AF019036	Synthetic
18	1155	80.4	1627	9	AK097350	Homo sapi
19	1155	80.4	1639	9	AK097350	Homo sapi
20	1148.2	79.9	1624	9	AK097206	Homo sapi
21	1147.2	79.8	1335	6	AX010615	Sequence
22	1147.2	79.8	1335	6	AX010646	Sequence
23	1141.4	79.4	1620	9	AK097366	Homo sapi
24	1140	79.3	1353	6	AX277242	Sequence
25	1139.8	79.3	1618	9	AK097360	Homo sapi
26	1138.6	79.2	1637	9	AK093636	Homo sapi
27	1133.4	78.9	1599	6	AX330501	Sequence
28	1133.4	78.9	1599	6	AX333307	Sequence
29	1133.4	78.9	1599	6	AX334122	Sequence
30	1133.4	78.9	1599	9	HUMIGHEPAH	Human (hybr
31	1132	78.8	1401	9	AF027159	Homo sapi
32	1131.8	78.8	1617	6	A29585	H. sapiens c
33	1127.4	78.5	1622	9	AK097359	Homo sapi
34	1127.4	78.5	9209	6	AR000007	Sequence
35	1127.4	78.5	9209	6	AR015961	Sequence
36	1127.4	78.5	9209	6	AR060920	Sequence
37	1127.4	78.5	9209	6	AR211052	Sequence
38	1127.4	78.5	9209	6	AX032414	Sequence
39	1127.4	78.5	9209	6	BD004714	Chimeric
40	1127.4	78.5	18986	6	AR051652	Sequence
41	1127.4	78.5	18986	6	AR092290	Sequence
42	1126.2	78.4	1465	10	S79307	IG gamma =i
43	1120.6	78.0	1404	6	AX268679	Sequence
44	1120.6	78.0	8120	6	AR116573	Sequence
45	1120.4	78.0	1628	9	AK097361	Homo sapi

ALIGNMENTS

RESULT 1
AR108865
LOCUS AR108865 1437 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6113898.
ACCESSION AR108865
VERSION AR108865.1 GI:12825141
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1437)
Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard, C.
Human B7.1-specific primatized antibodies and transfectomas
expressing said antibodies
Patent: US 6113898-A 7 05-SEP-2000;
JOURNAL

Pred. No. is the number of results predicted by chance to have a


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Db 144 FIFPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSIYSL 203
Qy 201 SSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 239
Db 204 SSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 242

RESULT 15
US-09-026-985-62
; Sequence 62, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-026-985-62

Query Match 75.4%; Score 936; DB 4; Length 242;
Best Local Similarity 81.7%; Pred. No. 1.8e-74;
Matches 179; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

Qy 21 EVVMTQSPSLSLPITTPGPASISCRSSQSLKHSNGDTFLSWYQKQKQPPRLIYKVSNRD 80
Db 24 DIQMTQSPSSLSASVGRVITTCRSSQSLVHGIGETYLHWYQKQKPKAPKLLIYKVSNR 83
Qy 81 SGVDPDRFSGSGAGTFTLKISAVEAEVGVYFCGCGTRTPTFGGKVEIKRTVAAPSV 140
Db 84 SGVPRFSGSGSGDFTLTISQPEDFATYCSQSTHVPFLTFPGQKVEIKRTVAAPSV 143
Qy 141 FIFPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSIYSL 200
Db 144 FIFPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSIYSL 203
Qy 201 SSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 239
Db 204 SSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 242
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Search completed: March 29, 2003, 09:17:41
Job time : 8.49182 secs

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 QY 120 PPIFGGKTKVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNAL 179
 Db 121 PLIFGGGKTKVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNAL 180
 QY 180 QSGNSQSVTEQSDKSTYSLSTLTLSKADYKHKVYACVTHOGLSSPVTYKSNRGE 239
 Db 181 QSGNSQSVTEQSDKSTYSLSTLTLSKADYKHKVYACVTHOGLSSPVTYKSNRGE 240

RESULT 13

US-09-049-672A-6
 ; Sequence 6, Application US/09049672A
 ; Patent No. 6135941
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Baughn, Mariah R.
 ; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/049,672A
 ; FILING DATE: HEREWITH
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cerrione, Michael C
 ; REGISTRATION NUMBER: 39,132
 ; REFERENCE/DOCKET NUMBER: PF-0497 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 234 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: COLSUCT01
 ; CLONE: 2280869
 ; US-09-049-672A-6

Query Match 75.6%; Score 939.5; DB 4; Length 234;
 Best Local Similarity 77.0%; Pred. No. 8.3e-75;
 Matches 184; Conservative 23; Mismatches 27; Indels 5; Gaps 2;
 QY 1 MSLPAQLGLLLLCVPGSSGEVVMQSPISLPITFGEPAISCRSSQSLKHSNGDTFLSW 60
 Db 1 MEAPQALLFELLWLPDSFGIEIWMQSPAIVSLSPGERATLSQASQSI----GST-IAM 55

QY 61 YQKGPQPRLLIYKVSNRDSGVDPFRSGSGAGTDTFTLKISAVEAEADVGVYFCQGT RTP 120
 Db 56 YQKGPQPRLLIYGASTRATGVPPFRSGSGTETFTLFISSLOEEDFALYYCQYKGP 115
 QY 121 PPIFGGKTKVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQ 180
 Db 116 LPIFGGKTRVQIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQ 175
 QY 181 QSGNSQSVTEQSDKSTYSLSTLTLSKADYKHKVYACVTHOGLSSPVTYKSNRGE 239
 Db 176 QSGNSQSVTEQSDKSTYSLSTLTLSKADYKHKVYACVTHOGLSSPVTYKSNRGE 234

RESULT 14

US-09-027-449-62
 ; Sequence 62, Application US/09027449
 ; Patent No. 6025158
 ; GENERAL INFORMATION:
 ; APPLICANT: Gonzalez, Tania R.
 ; APPLICANT: Leong, Steven R.
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
 ; NUMBER OF SEQUENCES: 72
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/027,449
 ; FILING DATE: 20-Feb-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/074,330
 ; FILING DATE: 22-Jan-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/038,664
 ; FILING DATE: 21-Feb-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Love, Richard B.
 ; REGISTRATION NUMBER: 34,659
 ; REFERENCE/DOCKET NUMBER: P1085R3-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-5530
 ; INFORMATION FOR SEQ ID NO: 62:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 242 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-09-027-449-62

Query Match 75.4%; Score 936; DB 3; Length 242;
 Best Local Similarity 81.7%; Pred. No. 1.8e-74;
 Matches 179; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 21 EVVMTQSPISLPITFGEPAISCRSSQSLKHSNGDTFTLSWYQKGPQPRLLIYKVSNRD 80
 Db 24 DIQMTQSPISLSASVGRVTITCRSSQSLVHGIGETVLYHWYQKPGKAPKLLIYKVSNR 83
 QY 81 SGVPRFSGSGAGTDTFTLKISAVEAEADVGVYFCQGT RTPPTPTFGGKTKVEIKRTVAAPSV 140
 Db 84 SGVPRFSGSGAGTDTFTLTSSLOEEDFALYYCQYKGP 143
 QY 141 FTFPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQSGNSQSVTEQSDKSTYSL 200

APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-121-952A-42

Query Match 78.6%; Score 976; DB 4; Length 242;
Best Local Similarity 84.5%; Pred. No. 5.6e-78;
Matches 185; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

QY 21 EVVMTQSPPLSPITGCEPASISCRSSQSLKHSNGDTFLSWYQKQGPPLLIYKVSNRD 80
DB 24 DIVMTQTPLSLPVSLGDAQISCRSSQSLVHGIGNTYLHWYLOKPGQSPKLLIYKVSNR 83
QY 81 SGVPRFSGSGAGTDTFLKISAVEAEDVGVFYFCGQGTPTPTFGGKVEIKRTVAAPSV 140
DB 84 SGVPRFSGSGGTDTFLIRSRVEAEDLGLYFCQSQSTHVPLTFGAGTKLEKRAVAAPTV 143
QY 141 FIPPPSDEQLKSGTASVVCLLNNFYPREAKQWKVDNALQSGNSQESVTEQDSKDYSL 200
DB 144 FIPPPSSEQLKSGTASVVCLLNNFYPREAKQWKVDNALQSGNSQESVTEQDSKDYSL 203
QY 201 SSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 239
DB 204 SSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 242

RESULT 11
US-09-234-340A-42
Sequence 42, Application US/09234340A
Patent No. 6468532
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsui, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-42

Query Match 78.6%; Score 976; DB 4; Length 242;
Best Local Similarity 84.5%; Pred. No. 5.6e-78;
Matches 185; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

QY 21 EVVMTQSPPLSPITGCEPASISCRSSQSLKHSNGDTFLSWYQKQGPPLLIYKVSNRD 80
DB 24 DIVMTQTPLSLPVSLGDAQISCRSSQSLVHGIGNTYLHWYLOKPGQSPKLLIYKVSNR 83
QY 81 SGVPRFSGSGAGTDTFLKISAVEAEDVGVFYFCGQGTPTPTFGGKVEIKRTVAAPSV 140
DB 84 SGVPRFSGSGGTDTFLIRSRVEAEDLGLYFCQSQSTHVPLTFGAGTKLEKRAVAAPTV 143
QY 141 FIPPPSDEQLKSGTASVVCLLNNFYPREAKQWKVDNALQSGNSQESVTEQDSKDYSL 200
DB 144 FIPPPSSEQLKSGTASVVCLLNNFYPREAKQWKVDNALQSGNSQESVTEQDSKDYSL 203
QY 201 SSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 239
DB 204 SSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 242

RESULT 12
US-09-301-593-36
Sequence 36, Application US/09301593A
Patent No. 6455677
GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Legier, Olivier
APPLICANT: Saidanna, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.189001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-301-593-36

Query Match 78.5%; Score 975.5; DB 4; Length 240;
Best Local Similarity 80.4%; Pred. No. 6.1e-78;
Matches 193; Conservative 18; Mismatches 28; Indels 1; Gaps 1;

QY 1 MSLPAQLGLLLICVPGSGEVVMTQSPPLSPITGCEPASISCRSSQSLKHS-NGDTFLS 59
DB 1 METDTLLWVLLWVPGSSGDIWMTQSPDLSAVSLGERATINCKSSQSLIYSRNQNYLA 60
QY 60 WYQKPGQPPRLIYKVSNRDVGVPDRFSGGAGTDTFLKISAVEAEDVGVFYFCGQGT 119

Qy 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGEC 239
Db 204 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGEC 242

RESULT 4
US-08-398-612A-56
; Sequence 56, Application US/08398612A
; Patent No. 5686070
; GENERAL INFORMATION:
; APPLICANT: Doershuk, Claire M.
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
; TREATMENT OF Inflammatory Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,612A
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398611
; FILING DATE: 01-MAR-1995
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P1
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-398-612A-56

Query Match 78.6%; Score 976; DB 1; Length 242;
Best Local Similarity 84.5%; Pred. No. 5.6e-78;
Matches 185; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

Qy 21 EVVMTQSLPLITPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPRLLIYKVSNRD 80
Db 24 DIVMTQPLSLPVLGDAQSISCRSSQSLVHGIGNTYLVHLYLQKPGQSPKLLIYKVSNR 83
Qy 81 SGVPDRFSGSGAGTDFTLTKISAVEAEDVGUYFCQGTRTPPTFGGKTKVEIKRTVAAPSV 140
Db 84 SGVPDRFSGSGGTDFTLRISRVEADLGLYFCQSTHVLPTFGAGTKLELKRAVAAPT 143
Qy 141 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSL 200
Db 144 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSL 203
Qy 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGEC 239

US-08-398-612A-56

Db 204 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGEC 242

RESULT 5
US-08-398-611A-56
; Sequence 56, Application US/08398611A
; Patent No. 5702946
; GENERAL INFORMATION:
; APPLICANT: Doershuk, Claire M.
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
; OF Inflammatory Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,611A
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P1
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-398-611A-56

Query Match 78.6%; Score 976; DB 1; Length 242;
Best Local Similarity 84.5%; Pred. No. 5.6e-78;
Matches 185; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

Qy 21 EVVMTQSLPLITPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPRLLIYKVSNRD 80
Db 24 DIVMTQPLSLPVLGDAQSISCRSSQSLVHGIGNTYLVHLYLQKPGQSPKLLIYKVSNR 83
Qy 81 SGVPDRFSGSGAGTDFTLTKISAVEAEDVGUYFCQGTRTPPTFGGKTKVEIKRTVAAPSV 140
Db 84 SGVPDRFSGSGGTDFTLRISRVEADLGLYFCQSTHVLPTFGAGTKLELKRAVAAPT 143
Qy 141 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSL 200
Db 144 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSL 203
Qy 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGEC 239

US-08-491-334A-56

QY 61 YQOKPGOPRLLIYKVNRSNDSVDRFSGSGAGTDFTLKISAVEAEDVGVYFCQGTTRP 120
 Db 61 YQOKPGOPRLLIYKVNRSNDSVDRFSGSGAGTDFTLKISAVEAEDVGVYFCQGTTRP 120
 QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
 Db 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
 QY 181 SGNQSQSVTEQDSKOSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 239
 Db 181 SGNQSQSVTEQDSKOSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 239

RESULT 2
 US-07-916-098A-56
 ; Sequence 56, Application US/07916098A
 ; Patent No. 5871732
 ; GENERAL INFORMATION:
 ; APPLICANT: BURKLY, LINDA C.
 ; APPLICANT: CHISHOLM, PATRICIA L.
 ; APPLICANT: THOMAS, DAVID W.
 ; APPLICANT: ROSA, MARGARET D.
 ; APPLICANT: ROSA, JOSEPH J.
 ; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
 ; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
 ; NUMBER OF SEQUENCES: 61
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
 ; STREET: 10 SOUTH WACKER DRIVE
 ; CITY: CHICAGO
 ; STATE: ILLINOIS
 ; COUNTRY: U.S.A.
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/916,098A
 ; FILING DATE: July 24, 1992
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/08843
 ; FILING DATE: No. 5871732ember 27, 1991
 ; CLASSIFICATION: 424
 ; APPLICATION NUMBER: 07/618,542
 ; FILING DATE: No. 5871732ember 27, 1990
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: JOHN J. MC DONNELL
 ; REGISTRATION NUMBER: 26,949
 ; REFERENCE/DOCKET NUMBER: 92,310-G
 ; TELEPHONE: (312) 715-1000
 ; TELEFAX: (312) 715-1234
 ; TELEX: 910/221-5317
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 241 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-916-098A-56

Query Match 78.7%; Score 978; DB 2; Length 241;
 Best Local Similarity 80.4%; Pred. No. 3.7e-78;
 Matches 193; Conservative 22; Mismatches 23; Indels 2; Gaps 2;

QY 1 MSIPAOGLGLLLICVPGSGEVMTQSPLSLPITPGEPASISCRSSOSLKHSG-NGDTFLS 59
 Db 3 MRVPAOGLGLLLWLPFGAGDIVMTQSPDSLAVSLGERATINCKSSGLSYSTINQNYLA 62

QY 60 WYQOKPGOPRLLIYKVNRSNDSVDRFSGSGAGTDFTLKISAVEAEDVGVYFCQGTTRT 119
 Db 63 WYQOKPGOPRLLIYKVNRSNDSVDRFSGSGAGTDFTLKISAVEAEDVGVYFCQGTTRT 121
 QY 120 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 179
 Db 122 YRTFGRGIKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 181
 QY 180 QSGNQSQSVTEQDSKOSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 239
 Db 182 QSGNQSQSVTEQDSKOSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 241

RESULT 3
 US-08-398-613A-56
 ; Sequence 56, Application US/08398613A
 ; Patent No. 5677426
 ; GENERAL INFORMATION:
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Hebert, Caroline Alice
 ; APPLICANT: Kim, Kyung Jin
 ; APPLICANT: Leong, Steven R.
 ; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory I
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/398,613A
 ; FILING DATE: 01-MAR-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/205864
 ; FILING DATE: 03-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitts, Renee A.
 ; REGISTRATION NUMBER: 35,136
 ; REFERENCE/DOCKET NUMBER: 874Pl-3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-1489
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 242 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-398-613A-56

Query Match 78.6%; Score 976; DB 1; Length 242;
 Best Local Similarity 84.5%; Pred. No. 5.6e-78;
 Matches 185; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

QY 21 EVVMTQSPLSLPITPGEPASISCRSSOSLKHSGNDTFLSWYQOKPGOPRLLIYKVNRS 80
 Db 24 DIVMTQSPLSLPVSLGDSQASISCRSSOSLVHGIGNTVLLHWYLOKPGOSKLLIYKVNRF 83
 QY 81 SGVPRFSGSGAGTDFTLKISAVEAEDVGVYFCQGTTRTPPTFGGTKEIKRTVAAPSV 140
 Db 84 SGVPRFSGSGAGTDFTLKISAVEAEDVGVYFCQGTTRTPPTFGGTKEIKRTVAAPSV 143
 QY 141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSL 200
 Db 144 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSL 203

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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:24 ; Search time 8.49182 Seconds
(without alignments)
828.100 Million cell updates/sec

Title: US-09-758-173-6

Perfect score: 1242

Sequence: 1 MSPLAQLGLLLCVPGSSG.....EVTHQGLSPVTKSFNRGEC 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCFUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	239	3	US-08-487-550-6
2	978	78.7	241	2	US-07-916-098A-56
3	976	78.6	242	1	US-08-398-613A-56
4	976	78.6	242	1	US-08-398-612A-56
5	976	78.6	242	1	US-08-398-611A-56
6	976	78.6	242	2	US-08-491-334A-56
7	976	78.6	242	3	US-09-027-449-42
8	976	78.6	242	3	US-08-804-444A-42
9	976	78.6	242	4	US-09-026-985-42
10	976	78.6	242	4	US-09-121-952A-42
11	976	78.6	242	4	US-09-234-340A-42
12	975.5	78.5	240	4	US-09-301-593-36
13	939.5	75.6	234	4	US-09-049-672A-6
14	936	75.4	242	3	US-09-027-449-62
15	936	75.4	242	4	US-09-036-985-62
16	936	75.4	242	4	US-09-121-952A-62
17	936	75.4	242	4	US-09-234-340A-62
18	935	75.3	242	3	US-09-027-449-51
19	935	75.3	242	3	US-08-804-444A-51
20	935	75.3	242	4	US-09-026-985-51
21	935	75.3	242	4	US-09-121-952A-51
22	935	75.3	242	4	US-09-234-340A-51
23	932	75.0	219	3	US-08-027-449-72
24	932	75.0	219	4	US-09-026-985-72
25	932	75.0	219	4	US-09-121-952A-72
26	932	75.0	219	4	US-09-234-340A-72
27	932	75.0	242	3	US-09-027-449-56

28	932	75.0	242	3	US-08-804-444A-56	Sequence 56, Appl
29	932	75.0	242	4	US-09-026-985-56	Sequence 56, Appl
30	932	75.0	242	4	US-09-121-952A-56	Sequence 56, Appl
31	932	75.0	242	4	US-09-234-340A-56	Sequence 56, Appl
32	928.5	74.8	240	4	US-09-301-593-28	Sequence 28, Appl
33	909.5	73.2	220	4	US-08-952-235-1	Sequence 1, Appl
34	909.5	73.2	220	4	US-09-669-971-1	Sequence 1, Appl
35	900.5	72.5	235	3	US-08-812-586-16	Sequence 16, Appl
36	900	72.5	235	1	US-08-276-852-153	Sequence 153, App
37	900	72.5	235	1	US-08-899-575-153	Sequence 153, App
38	900	72.5	235	1	US-08-899-575-153	Sequence 153, App
39	900	72.5	235	5	PCT-US95-08743-153	Sequence 5, Appl
40	899.5	72.4	236	5	US-08-157-101A-5	Sequence 5, Appl
41	893.5	71.9	218	5	PCT-US96-13152-2	Sequence 2, Appl
42	893.5	71.9	220	4	US-09-301-593-17	Sequence 17, Appl
43	888.5	71.5	233	2	US-07-934-373C-25	Sequence 25, Appl
44	888.5	71.5	233	3	US-08-437-642B-25	Sequence 25, Appl
45	888.5	71.5	233	4	US-08-146-206C-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-08-487-550-6

; Sequence 6, Application US/08487550

; Patent No. 6113898

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,550

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 6:

; LENGTH: 239 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-487-550-6

Query Match 100.0%; Score 1242; DB 3; Length 239;

Best Local Similarity 100.0%; Pred. No. 3.1e-101;

Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPLAQLGLLLCVPGSSGSEVMTQSPSLPITPGSPASISCRSSQSLKHSNGDTFLSW 60

Db 1 MSPLAQLGLLLCVPGSSGSEVMTQSPSLPITPGSPASISCRSSQSLKHSNGDTFLSW 60

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; PRIOR FILING DATE: 2000-11-17
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; PRIOR APPLICATION NUMBER: 60/249,297
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/231,242
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; PRIOR FILING DATE: 2000-09-08
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; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
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; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
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; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
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Query Match      87.8%; Score 1091; DB 26; Length 244;
Best Local Similarity 87.4%; Pred. No. 9,9e-85;
Matches 209; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

QY 1 MSLPAQLLGLLLCVPGSSGEVVMVTQSPLSLPIITPGEPASISCRSSQSLKHSNGDTFLSW 60
Db 6 MRLAQLLGLLLMLVPGSSGDIVMTQTPLSPVTLGQPASISCRSNQSLVHSDGNTYLSW 65

QY 61 YQKPGQPPRLIYKVSNRDVGVPDRFSGSGAGTDTFLKISAVEAEDVGVIYFCQGTRTP 120
Db 66 LQORFGQPPRLIYKISNRFSGVDPDRFSGSGAGTDTFLKITRVEAEDVGVIYCMQATQFP 125

QY 121 PTFGGGTKEIKRTVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
Db 126 LTFGGGTKEIQTVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 185

QY 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 186 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 244
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RESULT 15
US-09-760-479-658
; Sequence 658, Application US/09760479
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ53
; CURRENT APPLICATION NUMBER: US/09760,479
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 945
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 658
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-479-658
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Query Match      86.4%; Score 1073; DB 21; Length 262;
Best Local Similarity 87.0%; Pred. No. 3.8e-83;
Matches 208; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MSLPAQLLGLLLCVPGSSGEVVMVTQSPLSLPIITPGEPASISCRSSQSLKHSNGDTFLSW 60
Db 11 MRLPAQLLGLLLMLVPGSSGDIVMTQSPLSLPIITGQPASISCRSSQGLDGTGNTYLNW 70

QY 61 YQKPGQPPRLIYKVSNRDVGVPDRFSGSGAGTDTFLKISAVEAEDVGVIYFCQGTRTP 120
Db 71 FLQRPQSPRLIYKVSNRDVGVPDRFSGSGAGTDTFLKISAVEAEDVGVIYCMQGTHTP 130

QY 121 PTFGGGTKEIKRTVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
Db 131 YTFGGGTKEIKRTVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 190

QY 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 191 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 249
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Search completed: March 29, 2003, 09:34:12
Job time : 111.835 secs

; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
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; PRIOR FILING DATE: 2000-11-01
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; PRIOR FILING DATE: 2000-08-14
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; PRIOR FILING DATE: 2000-09-08
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; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
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; PRIOR APPLICATION NUMBER: 60/235,836
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; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
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; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,213
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,212
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,207
; PRIOR FILING DATE: 2000-11-17
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; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,244
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,217
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,211
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,215
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,264


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; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Takahashi, Tohru
; APPLICANT: Nakahara, Kaori
; APPLICANT: Yonehara, Shin
; TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY
; FILE REFERENCE: 980125/HG
; CURRENT APPLICATION NUMBER: US/09/046,351A
; CURRENT FILING DATE: 1998-03-23
; EARLIER APPLICATION NUMBER: JP HEI 9-67938
; EARLIER FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L chain of a
; OTHER INFORMATION: humanized anti-Fas antibody
US-09-046-351-82

Query Match      89.6%; Score 1113; DB 14; Length 239;
Best Local Similarity 90.0%; Pred. No. 1.3e-86;
Matches 215; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 MSPLPAQLLGLLLLCVPGSGGEVVMVTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MRLPAQLLGLLLMLWVPGSGDVVMVTQSPSLPITVTLGQPASISCRSSKSLVHSGNTYLHW 60

QY 61 YQKPGQPPRLLIYKVNRSRGVDPDRFSGSGAGTDFTLKISAVEAEDVGVPFCGQGRTP 120
Db 61 YLQKPGQPPRLLIYKVNRSRGVDPDRFSGSGAGTDFTLKISRVEAEDVGVIYCSQSTHVP 120

QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNALQ 180
Db 121 PAFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNALQ 180

QY 181 SGNQSQSVTEQDSKDYSLSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 239
Db 181 SGNQSQSVTEQDSKDYSLSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 239

RESULT 12
US-09-046-351-78
; Sequence 78, Application US/09046351A
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Takahashi, Tohru
; APPLICANT: Nakahara, Kaori
; APPLICANT: Yonehara, Shin
; TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY
; FILE REFERENCE: 980125/HG
; CURRENT APPLICATION NUMBER: US/09/046,351A
; CURRENT FILING DATE: 1998-03-23
; EARLIER APPLICATION NUMBER: JP HEI 9-67938
; EARLIER FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L chain of a
; OTHER INFORMATION: humanized anti-Fas antibody
US-09-046-351-78

Query Match      89.4%; Score 1110; DB 14; Length 239;
Best Local Similarity 89.5%; Pred. No. 2.3e-86;
Matches 214; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
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QY 1 MSPLPAQLLGLLLLCVPGSGGEVVMVTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MRLPAQLLGLLLMLWVPGSGDVVMVTQSPSLPITVTLGQPASISCRSSKSLVHSGNTYLHW 60

QY 61 YQKPGQPPRLLIYKVNRSRGVDPDRFSGSGAGTDFTLKISAVEAEDVGVPFCGQGRTP 120
Db 61 YLQKPGQSPKLLIYKVNRSRGVDPDRFSGSGAGTDFTLKISRVEAEDVGVIYCSQSTHVP 120

QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNALQ 180
Db 121 PAFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNALQ 180

QY 181 SGNQSQSVTEQDSKDYSLSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 239
Db 181 SGNQSQSVTEQDSKDYSLSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 239

RESULT 13
US-09-760-479-641
; Sequence 641, Application US/09760479
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT253
; CURRENT APPLICATION NUMBER: US/09/760,479
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 946
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 641
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-479-641

Query Match      87.8%; Score 1091; DB 21; Length 244;
Best Local Similarity 87.4%; Pred. No. 9.9e-85;
Matches 209; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

QY 1 MSPLPAQLLGLLLLCVPGSGGEVVMVTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
Db 6 MRLLAQLLGLLLMLWVPGSGDIWMTQTPLSSPVTLQGPASISCRSNQSLVHSDGNTYLSW 65

QY 61 YQKPGQPPRLLIYKVNRSRGVDPDRFSGSGAGTDFTLKISAVEAEDVGVPFCGQGRTP 120
Db 66 LQORPGQPPRLLIYKVNRSRGVDPDRFSGSGAGTDFTLKITRVEAEDVGVIYCMQATQFP 125

QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNALQ 180
Db 126 LTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNALQ 185

QY 181 SGNQSQSVTEQDSKDYSLSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 239
Db 186 SGNQSQSVTEQDSKDYSLSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 244

RESULT 14
US-10-206-008-641
; Sequence 641, Application US/10206008
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT253CIN
; CURRENT APPLICATION NUMBER: US/10/206,008
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 09/760,479
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
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MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/124,905
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/383,916
 FILING DATE:
 APPLICATION NUMBER: US 08/487,550
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Teskin, Robin L.
 REGISTRATION NUMBER: 35,030
 REFERENCE/DOCKET NUMBER: 012712-131
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-836-6620
 TELEFAX: 703-836-2021
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 239 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-10-124-905-6

Query Match 100.0%; Score 1242; DB 25; Length 239;
 Best Local Similarity 100.0%; Pred. No. 1.1e-97;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
 Db 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
 QY 61 YQKPGQPPRLIIYKVNRSQVDPFRFSGSGAGTDTFLKISAVEAEDVGVYFCQGGTRTP 120
 Db 61 YQKPGQPPRLIIYKVNRSQVDPFRFSGSGAGTDTFLKISAVEAEDVGVYFCQGGTRTP 120
 QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
 Db 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
 QY 181 SGNQSVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
 Db 181 SGNQSVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 9
 US-09-046-351-84
 ; Sequence 84, Application US/09046351A
 ; GENERAL INFORMATION:
 ; APPLICANT: Serizawa, Nobufusa
 ; APPLICANT: Haruyama, Hideyuki
 ; APPLICANT: Takahashi, Tohru
 ; APPLICANT: Nakahara, Kaori
 ; APPLICANT: Yonehara, Shin
 ; TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY
 ; FILE REFERENCE: 980125/HG
 ; CURRENT APPLICATION NUMBER: US/09/046,351A
 ; EARLIER FILING DATE: 1998-03-23
 ; EARLIER APPLICATION NUMBER: JP HEI 9-67938
 ; EARLIER FILING DATE: 1997-03-21
 ; NUMBER OF SEQ ID NOS: 189
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 84
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: L chain of a
 ; OTHER INFORMATION: humanized anti-Fas antibody

US-09-046-351-84
 Query Match 89.9%; Score 1116; DB 14; Length 239;
 Best Local Similarity 90.4%; Pred. No. 6.9e-87;
 Matches 216; Conservative 8; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
 Db 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
 QY 61 YQKPGQPPRLIIYKVNRSQVDPFRFSGSGAGTDTFLKISAVEAEDVGVYFCQGGTRTP 120
 Db 61 YQKPGQPPRLIIYKVNRSQVDPFRFSGSGAGTDTFLKISAVEAEDVGVYFCQGGTRTP 120
 QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
 Db 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
 QY 181 SGNQSVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
 Db 181 SGNQSVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 10
 US-09-046-351-80
 ; Sequence 80, Application US/09046351A
 ; GENERAL INFORMATION:
 ; APPLICANT: Serizawa, Nobufusa
 ; APPLICANT: Haruyama, Hideyuki
 ; APPLICANT: Takahashi, Tohru
 ; APPLICANT: Nakahara, Kaori
 ; APPLICANT: Yonehara, Shin
 ; TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY
 ; FILE REFERENCE: 980125/HG
 ; CURRENT APPLICATION NUMBER: US/09/046,351A
 ; EARLIER FILING DATE: 1998-03-23
 ; EARLIER APPLICATION NUMBER: JP HEI 9-67938
 ; EARLIER FILING DATE: 1997-03-21
 ; NUMBER OF SEQ ID NOS: 189
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 80
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: L chain of a
 ; OTHER INFORMATION: humanized anti-Fas antibody

Query Match 89.6%; Score 1113; DB 14; Length 239;
 Best Local Similarity 90.0%; Pred. No. 1.3e-86;
 Matches 215; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
 Db 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
 QY 61 YQKPGQPPRLIIYKVNRSQVDPFRFSGSGAGTDTFLKISAVEAEDVGVYFCQGGTRTP 120
 Db 61 YQKPGQPPRLIIYKVNRSQVDPFRFSGSGAGTDTFLKISAVEAEDVGVYFCQGGTRTP 120
 QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
 Db 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
 QY 181 SGNQSVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
 Db 181 SGNQSVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 11
 US-09-046-351-82
 ; Sequence 82, Application US/09046351A

;; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF
;; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;; STREET: 699 Prince Street
;; CITY: Alexandria
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22314

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/030,390
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/383,916
;; FILING DATE:
;; FILING DATE: 07-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Teskin, Robin L.
;; REGISTRATION NUMBER: 35,030
;; REFERENCE/DOCKET NUMBER: 012712-131
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-836-6620
;; TELEFAX: 703-836-6620
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 239 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-10-030-390-6

Query Match 100.0%; Score 1242; DB 24; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.1e-97;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSPLAQLGLLLCVPGSGEVVMTQSPISLPITGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MSPLAQLGLLLCVPGSGEVVMTQSPISLPITGEPASISCRSSQSLKHSNGDTFLSW 60
QY 61 YQKPGQPPRLIIYKVNRSNDSGVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCGGGTRTP 120
Db 61 YQKPGQPPRLIIYKVNRSNDSGVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCGGGTRTP 120
QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNALQ 180
Db 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNALQ 180
QY 181 SGNQSQSVTEQDSKSTYSLSSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 239
Db 181 SGNQSQSVTEQDSKSTYSLSSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 239

RESULT 7
US-10-124-807-6
; Sequence 6, Application US/10124807
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

;; STREET: 699 Prince Street
;; CITY: Alexandria
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22314
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/124,807
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/383,916
;; FILING DATE:
;; FILING DATE: 07-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Teskin, Robin L.
;; REGISTRATION NUMBER: 35,030
;; REFERENCE/DOCKET NUMBER: 012712-131
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-836-6620
;; TELEFAX: 703-836-2021
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 239 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-10-124-807-6

Query Match 100.0%; Score 1242; DB 25; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.1e-97;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSPLAQLGLLLCVPGSGEVVMTQSPISLPITGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MSPLAQLGLLLCVPGSGEVVMTQSPISLPITGEPASISCRSSQSLKHSNGDTFLSW 60
QY 61 YQKPGQPPRLIIYKVNRSNDSGVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCGGGTRTP 120
Db 61 YQKPGQPPRLIIYKVNRSNDSGVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCGGGTRTP 120
QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNALQ 180
Db 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNALQ 180
QY 181 SGNQSQSVTEQDSKSTYSLSSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 239
Db 181 SGNQSQSVTEQDSKSTYSLSSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 239

RESULT 8
US-10-124-905-6
; Sequence 6, Application US/10124905
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:

QY 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 4
US-09-758-173-6
; Sequence 6, Application US/09758173
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,173
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-6620
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-758-173-6

Query Match 100.0%; Score 1242; DB 21; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.le-97;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLLCVPGSSGEVMTQSPLSLPIPTGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MSLPAQLGLLLLCVPGSSGEVMTQSPLSLPIPTGEPASISCRSSQSLKHSNGDTFLSW 60

QY 61 YQOKPGQPPRLIIYKVNDRSGVDRFSGSGAGDTFTLKISAVEAEDVGVYFCQGTRTP 120
Db 61 YQOKPGQPPRLIIYKVNDRSGVDRFSGSGAGDTFTLKISAVEAEDVGVYFCQGTRTP 120

QY 121 PTFGGKTVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
Db 121 PTFGGKTVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180

QY 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 5
US-09-948-429B-6
; Sequence 6, Application US/09948429B
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-948-429B-6

Query Match 100.0%; Score 1242; DB 23; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.le-97;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLLCVPGSSGEVMTQSPLSLPIPTGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MSLPAQLGLLLLCVPGSSGEVMTQSPLSLPIPTGEPASISCRSSQSLKHSNGDTFLSW 60

QY 61 YQOKPGQPPRLIIYKVNDRSGVDRFSGSGAGDTFTLKISAVEAEDVGVYFCQGTRTP 120
Db 61 YQOKPGQPPRLIIYKVNDRSGVDRFSGSGAGDTFTLKISAVEAEDVGVYFCQGTRTP 120

QY 121 PTFGGKTVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
Db 121 PTFGGKTVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180

QY 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 6
US-10-030-390-6
; Sequence 6, Application US/10030390
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-383-916-6

Query Match 100.0%; Score 1242; DB 17; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.1e-97;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPTTPGEPASISCRSSQSLKHSNGDTFLSW 60
DB 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPTTPGEPASISCRSSQSLKHSNGDTFLSW 60
QY 61 YQKPGQPRLIIYKVNRSQVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCQGTTRTP 120
DB 61 YQKPGQPRLIIYKVNRSQVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCQGTTRTP 120
QY 121 PTFGGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
DB 121 PTFGGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
QY 181 SGNQSQSVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
DB 181 SGNQSQSVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 2

US-09-526-098-6
Sequence 6, Application US/09526098
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF"
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/09/526,098
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE: US 08/487,550
APPLICATION NUMBER: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-526-098-6

Query Match 100.0%; Score 1242; DB 19; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.1e-97;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPTTPGEPASISCRSSQSLKHSNGDTFLSW 60
DB 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPTTPGEPASISCRSSQSLKHSNGDTFLSW 60
QY 61 YQKPGQPRLIIYKVNRSQVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCQGTTRTP 120
DB 61 YQKPGQPRLIIYKVNRSQVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCQGTTRTP 120
QY 121 PTFGGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
DB 121 PTFGGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
QY 181 SGNQSQSVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
DB 181 SGNQSQSVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 3

US-09-576-424-6
Sequence 6, Application US/09576424
GENERAL INFORMATION:
APPLICANT: ANDERSON, DARRELL R.
APPLICANT: HANNA, NABIL
APPLICANT: BRAMS, PETER
APPLICANT: HEARD, CHERYL
TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
TITLE OF INVENTION: CO-STIMULATORY ANTIGENS
FILE REFERENCE: 37003-275681
CURRENT APPLICATION NUMBER: US/09/576,424
CURRENT FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US97/19906
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 08/746,361
PRIOR FILING DATE: 1996-11-08
PRIOR APPLICATION NUMBER: 08/487,550
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 6
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-09-576-424-6

Query Match 100.0%; Score 1242; DB 19; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.1e-97;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPTTPGEPASISCRSSQSLKHSNGDTFLSW 60
DB 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPTTPGEPASISCRSSQSLKHSNGDTFLSW 60
QY 61 YQKPGQPRLIIYKVNRSQVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCQGTTRTP 120
DB 61 YQKPGQPRLIIYKVNRSQVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCQGTTRTP 120
QY 121 PTFGGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
DB 121 PTFGGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180

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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:10:32 ; Search time 109.835 Seconds
(without alignments)
1402.934 Million cell updates/sec

Title: US-09-758-173-6

Perfect score: 1242
Sequence: 1 MSLPQALLGILLVCPOSSG.....EVTHQGLSPVTKSPNRGEC 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:*

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21: /cgn2_6/ptodata/1/paa/US09 COMB.pcp.*
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23: /cgn2_6/ptodata/1/paa/US09 COMB.pcp.*
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25: /cgn2_6/ptodata/1/paa/US09 COMB.pcp.*
26: /cgn2_6/ptodata/1/paa/US09 COMB.pcp.*
27: /cgn2_6/ptodata/1/paa/US09 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	239	17	US-09-383-916-6
2	1242	100.0	239	19	US-09-526-098-6
3	1242	100.0	239	19	US-09-576-424-6
4	1242	100.0	239	21	US-09-758-173-6
5	1242	100.0	239	23	US-09-948-429B-6
6	1242	100.0	239	24	US-10-030-390-6

7	1242	100.0	239	25	US-10-124-807-6
8	1242	100.0	239	25	US-10-124-905-6
9	1116	89.9	239	14	US-09-046-351-84
10	1113	89.6	239	14	US-09-046-351-80
11	1113	89.6	239	14	US-09-046-351-82
12	1110	89.4	239	14	US-09-046-351-78
13	1091	87.8	244	21	US-09-760-479-641
14	1091	87.8	244	26	US-10-206-008-641
15	1073	86.4	262	21	US-09-760-479-658
16	1073	86.4	262	26	US-10-206-008-658
17	1070.5	86.2	239	1	PCT-US02-11854A-19
18	1069	86.1	239	25	US-10-108-260A-4028
19	1068	86.0	239	23	US-09-924-340-8
20	1068	86.0	239	23	US-09-992-600A-8
21	1068	86.0	239	23	US-09-994-590-8
22	1068	86.0	239	24	US-10-000-489-8
23	1068	86.0	239	24	US-10-000-986-8
24	1068	86.0	239	27	US-60-305-456-8
25	1052.5	84.7	238	11	US-08-721-612B-19
26	1052.5	84.7	238	11	US-08-721-612C-19
27	1052.5	84.7	238	11	US-08-721-612D-19
28	1052.5	84.7	238	11	US-08-721-612E-19
29	1042	83.9	241	22	US-09-831-805A-15
30	1042	83.9	241	27	US-60-128-194-1
31	1041	83.8	239	1	PCT-US02-11853-19
32	1033	83.2	219	1	PCT-US02-11854A-11
33	1014	81.6	217	21	US-09-791-537-116780
34	1011	81.4	217	21	US-09-791-537-116791
35	1009	81.2	219	1	PCT-US02-21323-11
36	1009	81.2	219	1	PCT-US02-21324-11
37	1009	81.2	219	1	PCT-US02-26321-11
38	1008	81.2	219	23	US-09-972-656-92
39	1007	81.1	238	24	US-10-031-355-2
40	1007	81.1	238	24	US-10-031-355-11
41	1007	81.1	238	24	US-10-031-355-13
42	1007	81.1	238	24	US-10-031-355-15
43	1004	80.8	219	1	PCT-US02-11853-11
44	997	80.3	219	23	US-09-972-656-106
45	992.5	79.9	220	22	US-09-822-698A-24

ALIGNMENTS

RESULT 1

US-09-383-916-6
; Sequence 6, Application US/09383916
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/383,916
; FILING DATE: 26-AUG-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995

INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
US-09-726-258-72

Query Match 75.0%; Score 932; DB 9; Length 219;
Best Local Similarity 81.7%; Pred. No. 6.1e-40;
Matches 179; Conservative 14; Mismatches 26; Indels 0; Gaps 0;
QY 21 EYVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQKQKPGQPPRLIIYKVSNRD 80
DB 1 DIQMTQSPSSLSASVGRVITTCRSSQSLVHGIGATYLVHWYQKQKAPKLLIYKVSNR 60
QY 81 SGVPRFSGSGAGTDFTLKISAVEAEADVGVYFCGQGTPTPTFGGTTKVEIKRTVAAPSV 140
DB 61 SGVPSRFSGSGGTDFLTITSLQPEDFATYYCSQSTHVPLTFGQGTVEIKRTVAAPSV 120
QY 141 FIFPDSQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
DB 121 FIFPDSQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
DB 181 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 219

RESULT 15
US-09-726-258-56
Sequence 56, Application US/09726258
Publication No. US20030021790A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hse, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/094003
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/425-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:

LENGTH: 242 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
US-09-726-258-56

Query Match 75.0%; Score 932; DB 9; Length 242;
Best Local Similarity 81.7%; Pred. No. 6.6e-40;
Matches 179; Conservative 14; Mismatches 26; Indels 0; Gaps 0;
QY 21 EYVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQKQKPGQPPRLIIYKVSNRD 80
DB 24 DIQMTQSPSSLSASVGRVITTCRSSQSLVHGIGATYLVHWYQKQKAPKLLIYKVSNR 83
QY 81 SGVPRFSGSGAGTDFTLKISAVEAEADVGVYFCGQGTPTPTFGGTTKVEIKRTVAAPSV 140
DB 84 SGVPSRFSGSGGTDFLTITSLQPEDFATYYCSQSTHVPLTFGQGTVEIKRTVAAPSV 143
QY 141 FIFPDSQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
DB 144 FIFPDSQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 203
QY 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
DB 204 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 242

Search completed: March 29, 2003, 09:38:39
Job time: 11.1622 secs

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;
; REFERENCE/DOCKET NUMBER: P1085R4-1A
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/245-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-726-258-62

```

Query Match 75.4%; Score 936; DB 9; Length 242;
Best Local Similarity 81.7%; Pred. NO. 4.2e-40;
Matches 179; Conservative 15; Mismatches 25; Indels

[illegible]

RESULT 13
US-09-726-258-51

```

1  Sequence 51, Application US/09726258
2  Publication No. US20030021790A1
3  GENERAL INFORMATION:
4  APPLICANT: Genentech, Inc., Hsei, Vanessa
5  APPLICANT: Komenig, Iphigenia
6  APPLICANT: Leong, Steven R.
7  APPLICANT: Presta, Leonard G.
8  APPLICANT: Shahrokh, Zahra
9  APPLICANT: Zapata, Gerardo A.
10 TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER
11 TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONO
12 NUMBER OF SEQUENCES: 72
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: Genentech, Inc.
15 STREET: 1 DNA Way
16 CITY: South San Francisco
17 STATE: California
18 COUNTRY: USA
19 ZIP: 94080
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
22 COMPUTER: IBM PC compatible
23 OPERATING SYSTEM: PC-DOS/MS-DOS
24 SOFTWARE: WinPatIn (Genentech)
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/09/726,258
27 FILING DATE:
28 CLASSIFICATION:
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: 09/234,182
31 FILING DATE:
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: 60/094003
34 FILING DATE: 24-JUL-1998
35 ATTORNEY/AGENT INFORMATION:
36 NAME: Love, Richard B.
37 REGISTRATION NUMBER: 34,659
38 REFERENCE/DOCKET NUMBER: P1085R4-1A
39 TELECOMMUNICATION INFORMATION:

```

```

;      TELEPHONE: 650/295-5530
;      TELEFAX: 650/952-9881
;      INFORMATION FOR SEQ ID NO: 51:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 242 amino acids
;      TYPE: Amino Acid
;      TOPOLOGY: Linear
US-09-726-259-51

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Query Match 75.3%; Score 935; DB 9; Length 242;
Best Local Similarity 81.7%; Pred. No. 4.7e-40;
Matches 179; Conservative 15; Mismatches 25; Indels

[illegible]

RESULT 14
US-09-726-258-72

Sequence 72, Application US/09726259
Publication No. US20030021790A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokhi, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,259
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/094003
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: F1085R4-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881

```
QY 60 WYQKPGQPPRLIIYKVNRSQVDPDRFSGSGAGTDTFTLKISAVEAEDVGVYFCGGTGT 119
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
Db 61 WYQKPGQPPKLLIYWASTRSGVDPDRFSGSGGTDTFTLTISLQADVAVYCCQYYGT 120
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
QY 120 PPTFGGKTVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL 179
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
Db 121 PYSFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 236
; TYPE: PRT
QY 180 QSGNSQESVTEQDSKDYSLSTLTKSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
; ORGANISM: Homo sapiens
Db 181 QSGNSQESVTEQDSKDYSLSTLTKSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
; US-09-859-053-38

RESULT 10
US-09-859-053-34
; Sequence 34, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-34

Query Match 76.1%; Score 945.5; DB 10; Length 236;
Best Local Similarity 77.1%; Pred. No. 1.4e-40;
Matches 185; Conservative 25; Mismatches 25; Indels 5; Gaps 2;
GENERAL INFORMATION:
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658A1uaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-053-34

QY 1 MSLPAQLGLLLLCVPGSSGEVMTQSPSLPITPGEPAISCRSSQSLKSHNGDTFLSW 60
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
Db 1 METPAQLFLLLWLPTTGEIVLTQSPGTLSPGERATLSCRASQINRSS---YLAW 56
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
QY 61 YQKPGQPPRLIIYKVNRSQVDPDRFSGSGAGTDTFTLKISAVEAEDVGVYFCGQ-GTGT 119
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
Db 57 YQKPGQAPGLLIYGASRATGIPDRFSGSGGTDTFTLTISRLPEDFAVYYCQFGSSP 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-34

Query Match 76.1%; Score 945.5; DB 10; Length 236;
Best Local Similarity 77.1%; Pred. No. 1.4e-40;
Matches 185; Conservative 25; Mismatches 25; Indels 5; Gaps 2;
GENERAL INFORMATION:
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658A1uaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-053-34

QY 1 MSLPAQLGLLLLCVPGSSGEVMTQSPSLPITPGEPAISCRSSQSLKSHNGDTFLSW 60
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
Db 1 METPAQLFLLLWLPTTGEIVLTQSPGTLSPGERATLSCRASQINRSS---YLAW 56
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
QY 61 YQKPGQPPRLIIYKVNRSQVDPDRFSGSGAGTDTFTLKISAVEAEDVGVYFCGQ-GTGT 119
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
Db 57 YQKPGQAPGLLIYGASRATGIPDRFSGSGGTDTFTLTISRLPEDFAVYYCQFGSSP 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-34

Query Match 76.1%; Score 945.5; DB 10; Length 236;
Best Local Similarity 77.1%; Pred. No. 1.4e-40;
Matches 185; Conservative 24; Mismatches 26; Indels 5; Gaps 2;
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsai, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/094003
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
```

US-09-726-258-42

Query Match 78.6%; Score 976; DB 9; Length 242;
Best Local Similarity 84.5%; Pred. No. 4.4e-42;
Matches 185; Conservative 16; Mismatches 18; Indels 0; Gaps 0;
Qy 21 EVVMTQSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQKQKQPPRLLIYKVSNRD 80
Db 24 DIVMTQTLPSVLGDAQSISCRSSQSLVHGIGNYLLHWYLOKQKQSLLIYKVSNEF 83
Qy 81 SGVDFRSGSGAGTDFTLKISAVEADVGIVFCQGTTRTPPTFGGKVEIKRTVAAPSV 140
Db 84 SGVDFRSGSGGCTDFTLRISRVEADLGLYFCQSTHVPFTFGAGTKLEKRAVAAPTV 143
Qy 141 FIPPPDEQLKSGTASVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYSL 200
Db 144 FIPPPSEQLKSGTASVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYSL 203
Qy 201 SSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 239
Db 204 SSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 242

RESULT 7
US-09-909-567B-50
; Sequence 50, Application US/09909567B
; Publication No. US2003002257A1
; GENERAL INFORMATION:
; APPLICANT: Macine, Roberto A.
; APPLICANT: Nair, Manoj
; APPLICANT: Chen, Seiyu
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
; FILE REFERENCE: DEX-0214
; CURRENT APPLICATION NUMBER: US/09/909,567B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/219,834
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-909-567B-50

Query Match 77.3%; Score 960.5; DB 9; Length 228;
Best Local Similarity 83.5%; Pred. No. 2.5e-41;
Matches 187; Conservative 17; Mismatches 19; Indels 1; Gaps 1;
Qy 17 GSGGEVMTQSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQKQKQPPRLLIYKV 76
Db 5 GPACAEIVMTQTLPSLITPGEQASMSCRSSQSLHSDGYTYLYWFLQKQSPQLLIYEV 64
Qy 77 SNRDSGV-PDRFSGSGAGTDFTLKISAVEADVGIVFCQGTTRTPPTFGGKVEIKRTV 135
Db 65 SNRFGVSPTRFSGSGRGFTLRISRVEADAGVYVCMQTQTPTFGQGTLEIKRTV 124
Qy 136 AAPSVTFIPPSDQLKSGTASVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKD 195
Db 125 AAPSVTFIPPSDQLKSGTASVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKD 184
Qy 196 STYLSSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 239
Db 185 STYLSSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 228

RESULT 8
US-09-249-011A-22
; Sequence 22, Application US/09249011A
; Patent No.: US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO

; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-249-011A-22

Query Match 77.3%; Score 960; DB 9; Length 239;
Best Local Similarity 79.6%; Pred. No. 2.7e-41;
Matches 191; Conservative 20; Mismatches 27; Indels 2; Gaps 2;
Qy 1 MSLPAQLGLLLLCVPGSSGEVMTQSLPITPGEPASISCRSSQSLKHS-NGDTFLS 59
Db 1 MDSQAQLVILLLLWVSGTCGDIVLTQSPDLSVLSGERATISCKSSQSLNSRTRENYLA 60
Qy 60 WYQKQKQPPRLLIYKVSNRDVGVPDRFSGSGAGTDFTLKISAVEADVGIVFCQGTTRT 119
Db 61 WYQKQKQPPKLLIYMASTRESGVDFRFGSGSGTDFTLTISSLOAEDVAVYVCSQSYNL 120
Qy 120 PPTFGGKVEIKRTVAAPSVTFIPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNAL 179
Db 121 -YTFGQGTKEIKRTVAAPSVTFIPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNAL 179
Qy 180 QSGNSQESVTEQDSKSTYLSSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 239
Db 180 QSGNSQESVTEQDSKSTYLSSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 239

RESULT 9
US-09-799-514-8
; Sequence 8, Application US/09799514
; Patent No. US20020065220A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and Ant
; FILE REFERENCE: PT015P1
; CURRENT APPLICATION NUMBER: US/09/799,514
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/US00/23662
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/152,248
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-514-8

Query Match 76.9%; Score 954.5; DB 10; Length 240;
Best Local Similarity 77.5%; Pred. No. 5.1e-41;
Matches 186; Conservative 26; Mismatches 27; Indels 1; Gaps 1;
Qy 1 MSLPAQLGLLLLCVPGSSGEVMTQSLPITPGEPASISCRSSQSLKHSNGD-TFLS 59
Db 1 MVLQTQVFISLLLMISGAYDIVMTQSPDLSVLSGERATINCKSSQTVLYSSDNKNYLA 60

```
US-09-992-600A-8
; Sequence 8, Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Benjanin, Stephanie
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US4.DIV
; CURRENT APPLICATION NUMBER: US/09/992,600A
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: JPatent
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..20
; US-09-992-600A-8

Query Match      86.0%; Score 1068; DB 9; Length 239;
Best Local Similarity 86.6%; Pred. No. 1.2e-46;
Matches 207; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 MSLPAGLLGLLLCVPGSGSEVVMQSPISLPITPGEPAISCRSSQSLKHNGDFTLSW 60
DB 1 MRLPAQLGLGLMLVWSSGSDIVMTQSPILFVPTPGEPAISCRSSQSLHVVQGSNYLDW 60
QY 61 YQKPGQPRLLYKYVNRDSVDPDRFSGSGAGTDTLTKISAVEADVGVYFCGGCTRT 120
DB 61 YHOKPGSPQLLYLGSNRASGVDRFSGSGGTDTLTKISRVEADVGVYCMQALQTP 120
QY 121 PTFGGTQKVEIKRTVAAPSVFIFPPSDEQLKSGTASVIVCLNNFYPREAKVQKVDNALQ 180
DB 121 FTGPGTRVDIKRTVAAPSVFIFPPSDEQLKSGTASVIVCLNNFYPREAKVQKVDNALQ 180
QY 181 SGNQSSEVTEQDSKDYSLSSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNREGC 239
DB 181 SGNQSSEVTEQDSKDYSLSSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNREGC 239

RESULT 5
US-09-822-698A-24
; Sequence 24, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 24
; LENGTH: 220
; TYPE: PRT
; ORGANISM: artificial sequence

; FEATURE:
; OTHER INFORMATION: immunoglobulin kappa light chain of MUC1-specific PH1-IgG1
US-09-822-698A-24

Query Match      79.9%; Score 992.5; DB 10; Length 220;
Best Local Similarity 87.7%; Pred. No. 6.3e-43;
Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 21 EVVMTQSPISLPITPGEPAISCRSSQSLKHNGDFTLSWYQKPGQPPRLLYKYVSNRD 80
DB 1 EIVLTQSPISLPVTPGEPAISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLYYSGSHRA 60
QY 81 SGVDPDRFSGSGAGTDTLTKISAVEADVGVYFCGGCTRTPTTGGTQKVEIKR-TVAAPS 139
DB 61 SGVDPDRFSGSVSGTDTLTKISRVEADVGVYCMQGLSPFTFGPGTKVDIKKGTVAAPS 120
QY 140 VFIFPPSDEQLKSGTASVIVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 199
DB 121 VFIFPPSDEQLKSGTASVIVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
QY 200 LSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNREGC 239
DB 181 LSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNREGC 220

RESULT 6
US-09-726-258-42
; Sequence 42, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-124-905-6

Query Match 100.0%; Score 1242; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.1e-55;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLLCVPGSGGVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
DB 1 MSLPAQLGLLLLCVPGSGGVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60

QY 61 YQKPGQPPRLIIYKVSNRDGVDPDRFGSGAGTDFTLKISAVEAEDGVYFCQGTRTP 120
DB 61 YQKPGQPPRLIIYKVSNRDGVDPDRFGSGAGTDFTLKISAVEAEDGVYFCQGTRTP 120

QY 121 PTFGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180
DB 121 PTFGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180

QY 181 SGNQSVTEQDSKOSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC 239
DB 181 SGNQSVTEQDSKOSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC 239

RESULT 2
US-09-948-429B-6
Sequence 6, Application US/09948429B
Patent No. US2002017769A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-948-429B-6

Query Match 100.0%; Score 1242; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.1e-55;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLLCVPGSGGVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
DB 1 MSLPAQLGLLLLCVPGSGGVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60

QY 61 YQKPGQPPRLIIYKVSNRDGVDPDRFGSGAGTDFTLKISAVEAEDGVYFCQGTRTP 120
DB 61 YQKPGQPPRLIIYKVSNRDGVDPDRFGSGAGTDFTLKISAVEAEDGVYFCQGTRTP 120

QY 121 PTFGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180
DB 121 PTFGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180

QY 181 SGNQSVTEQDSKOSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC 239
DB 181 SGNQSVTEQDSKOSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC 239

RESULT 3
US-09-924-340-8
Sequence 8, Application US/09924340
Publication No. US20030027248A1
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91 US2 REG
CURRENT APPLICATION NUMBER: US/09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 8
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: 1..20
US-09-924-340-8

Query Match 86.0%; Score 1068; DB 9; Length 239;
Best Local Similarity 86.6%; Pred. No. 1.2e-46;
Matches 207; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLLCVPGSGGVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
DB 1 MSLPAQLGLLLLCVPGSGGVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60

QY 61 YQKPGQPPRLIIYKVSNRDGVDPDRFGSGAGTDFTLKISAVEAEDGVYFCQGTRTP 120
DB 61 YQKPGQPPRLIIYKVSNRDGVDPDRFGSGAGTDFTLKISAVEAEDGVYFCQGTRTP 120

QY 121 PTFGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180
DB 121 PTFGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180

QY 181 SGNQSVTEQDSKOSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC 239
DB 181 SGNQSVTEQDSKOSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC 239

RESULT 4

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:14:52 ; Search time 9.16222 Seconds
(without alignments)
1531.829 Million cell updates/sec

Title: US-09-758-173-6

Perfect score: 1242

Sequence: 1 MSIPALLGLLLCVPGSSG.....EVTHQGLSPVTKSNRGC 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pdb.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pdb.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pdb.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1242	100.0	239	9 US-10-124-905-6	Sequence 6, Appli
2	1242	100.0	239	9 US-09-948-429B-6	Sequence 6, Appli
3	1068	86.0	239	9 US-09-924-340-8	Sequence 8, Appli
4	1068	86.0	239	9 US-09-992-600A-8	Sequence 8, Appli
5	992.5	79.9	220	10 US-09-822-698A-24	Sequence 24, Appl
6	976	78.6	242	9 US-09-726-258-42	Sequence 42, Appl
7	960.5	77.3	228	9 US-09-909-567B-50	Sequence 50, Appl
8	960	77.3	239	9 US-09-249-011A-22	Sequence 22, Appl
9	954.5	76.9	242	10 US-09-799-514-8	Sequence 8, Appli
10	945.5	76.1	236	10 US-09-859-053-34	Sequence 34, Appl
11	940.5	75.7	236	10 US-09-859-053-38	Sequence 38, Appl
12	936	75.4	242	9 US-09-726-258-62	Sequence 62, Appl
13	935	75.3	242	9 US-09-726-258-51	Sequence 51, Appl
14	932	75.0	219	9 US-09-726-258-72	Sequence 72, Appl
15	932	75.0	242	9 US-09-726-258-56	Sequence 56, Appl
16	924.5	74.4	236	10 US-09-859-053-30	Sequence 30, Appl
17	909.5	73.2	220	10 US-09-995-693-1	Sequence 1, Appli
18	904.5	72.8	234	10 US-09-740-002-24	Sequence 24, Appl
19	901.5	72.6	236	9 US-10-006-593-69	Sequence 69, Appl

20 898.5 72.3 239 10 US-09-825-012-9 Sequence 9, Appli
21 893.5 71.9 218 10 US-09-917-410-2 Sequence 2, Appli
22 892.5 71.9 218 9 US-09-925-179-67 Sequence 67, Appli
23 892.5 71.9 220 10 US-09-917-410-5 Sequence 5, Appli
24 887 71.4 242 9 US-09-479-614-20 Sequence 20, Appli
25 885.5 71.3 218 9 US-09-925-179-9 Sequence 9, Appli
26 885.5 71.3 218 10 US-09-802-077-9 Sequence 9, Appli
27 885.5 71.3 218 10 US-09-802-096-9 Sequence 13, Appli
28 885.5 71.3 218 10 US-09-920-171-13 Sequence 2, Appli
29 883.5 71.1 214 10 US-09-940-166A-2 Sequence 11, Appli
30 883.5 71.1 214 10 US-09-811-384-11 Sequence 6, Appli
31 883.5 71.1 237 10 US-09-940-166A-6 Sequence 150, Appli
32 880.5 70.9 234 10 US-09-800-729-150 Sequence 97, Appli
33 880 70.9 235 10 US-09-910-059-97 Sequence 152, Appli
34 879 70.8 235 10 US-09-800-729-152 Sequence 52, Appli
35 877 70.6 235 10 US-09-910-059-52 Sequence 5, Appli
36 876.5 70.5 212 12 US-10-011-135-5 Sequence 15, Appli
37 875.5 70.5 218 10 US-09-920-171-15 Sequence 17, Appli
38 875.5 70.5 218 10 US-09-920-171-17 Sequence 19, Appli
39 875.5 70.5 218 10 US-09-920-171-19 Sequence 24, Appli
40 875.5 70.5 218 10 US-09-920-171-24 Sequence 26, Appli
41 875 70.5 234 10 US-09-740-002-26 Sequence 118, Appli
42 874.5 70.4 212 9 US-10-006-593-118 Sequence 26, Appli
43 871 70.1 235 10 US-09-910-059-99 Sequence 99, Appli
44 865 69.6 235 10 US-09-910-059-17 Sequence 17, Appli
45 857 69.0 669 9 US-09-807-721-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-124-905-6

; Sequence 6, Application US/10124905

; Patent No. US20020166136A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM: Floppy disk

; MEDIUM TYPE: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/124,905

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/383,916

; FILING DATE:

; APPLICATION NUMBER: US 08/487,550

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 239 amino acids

PT including metastasis, and pain
XX
PS Claim 31; Page 34-35; 88pp; Japanese.

XX The present invention describes a human monoclonal antibody to
CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC its fragments, following the stimulation of PTHrP has the following
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment
CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingiva sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a
CC human PTHrP monoclonal antibody clone protein sequence from the
CC present invention.

XX Sequence 239 AA;

Query Match 85.7%; Score 1065; DB 21; Length 239;
Best Local Similarity 85.8%; Pred. No. 1.5e-58;
Matches 205; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLCVPGSGEVVMTQSPSLPITPGEPASISCRSSQSLKHNGDTFLSW 60

DB 1 MRLPAQLGLLMLVWSSGSDIVMTQSPSLPVTGPATISCRSSQSLHNGNLYDW 60

QY 61 YQKPGQPPRLIIYKVNRSRSGVDPDRFSGSGAGTDTFLKISAVEAEDVGYFCGGQTRTP 120

DB 61 FLQKPGSQPLLIIYLGNSRASGVDPDRFSGSGGTDTFLKSRVEAEDVGLYYCMQALQIP 120

QY 121 PTFGGGTKEIKRTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQ 180

DB 121 FTFGPGTKVDIKRTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQ 180

QY 181 SGNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

DB 181 SGNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

RESULT 14

AA82610

ID AAY82610 standard; Protein; 239 AA.

XX AC AAY82610;

XX 02-AUG-2000 (first entry)

XX Human PTHrP monoclonal antibody clone 15H7-8-3 protein SEQ ID NO:4.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys

FT Misc-difference 156 /label= Phe, Ser, Tyr, Cys

FT Misc-difference 164 /label= Phe, Leu

FT JP2000080100-A.

XX 21-MAR-2000.

XX 12-OCT-1998; 98JP-0304793.

PR 17-JUN-1998; 98JP-0188196.
PR 26-JUN-1998; 98JP-0196729.

XX (NISB) JAPAN TOBACCO INC.

XX WPI: 2000-286723/25.

XX N-PSDB; AAA13920.

PT A human monoclonal antibody to parathyroid hormone related protein. -
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain

XX Claim 31; Page 33; 88pp; Japanese.

XX The present invention describes a human monoclonal antibody to
CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC its fragments, following the stimulation of PTHrP has the following
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment
CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingiva sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a
CC human PTHrP monoclonal antibody clone protein sequence from the
CC present invention.

XX Sequence 239 AA;

Query Match 85.8%; Score 1063; DB 21; Length 239;

Best Local Similarity 86.2%; Pred. No. 1.9e-58;

Matches 206; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLCVPGSGEVVMTQSPSLPITPGEPASISCRSSQSLKHNGDTFLSW 60

DB 1 MRLPAQLGLLMLVWSSGSDIVMTQSPSLPVTGPATISCRFSQSLHNSNGNLYDW 60

QY 61 YQKPGQPPRLIIYKVNRSRSGVDPDRFSGSGAGTDTFLKISAVEAEDVGYFCGGQTRTP 120

DB 61 YLQKPGSQPLLIIYLGNSRASGVDPDRFSGSGGTDTFLKISRVEAEDVGYVCMQALQTP 120

QY 121 PTFGGGTKEIKRTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQ 180

DB 121 FTFGPGTKVDIKRTVAAPSVFIPPPSDEQLKSGTAXVCLNNXYPREAKVQWKVDNALQ 180

QY 181 SGNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

DB 181 SGNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

RESULT 15

AA82617

ID AAY82617 standard; Protein; 239 AA.

XX AC AAY82617;

XX 02-AUG-2000 (first entry)

XX Human PTHrP monoclonal antibody clone 3G4-3 protein SEQ ID NO:18.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

XX Homo sapiens.

XX Key Location/Qualifiers

PH Misc-difference 3 /label= Phe, Leu, Ile, Val

FT Misc-difference 4

CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).
 CC Primers specific for the anti-human Fas antibody, light, heavy and kappa
 CC chains used in the invention are represented by sequences
 CC AAA78213-A78266. Primers used for sequencing the human Ig DNA used in the
 CC invention are represented by sequences AAA78277-A78318 and
 CC AAA78335-A78337, while humanised anti-Fas Ig DNA sequencing primers are
 CC represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer
 CC sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in
 CC the production of the agent of the invention.

XX SQ Sequence 239 AA;

Query Match 89.4%; Score 1110; DB 21; Length 239;
 Best Local Similarity 89.5%; Pred. No. 2.4e-61;
 Matches 214; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 MSPLPAQLLGLLLCVSGSGEVMTQSPSLPTTPGPASISCRSSQSLKHSNGDTFLSW 60
 DB 1 MRLPAQLLGLLMLVPGSGDVMTQSPSLPTVLGPASISCRSSKSLVHSGNTYLHW 60
 QY 61 YQKPGOPPRLLIYKSNRDSGVDPDRFSGSGAGTDFTLKISAVEAEDVGVFSGGQTRTP 120
 DB 61 YLQKPGQPKLLIYKSNRDSGVDPDRFSGSGAGTDFTLKISAVEAEDVGVFCSGTHVP 120
 QY 121 PTGGGQTKVEIKRTVAAPSFIIPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQ 180
 DB 121 PAFGQGTKEIKRTVAAPSFIIPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQ 180
 QY 181 SGNSQSVTEQDSKDYSLSSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239
 DB 181 SGNSQSVTEQDSKDYSLSSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 12

AA82615
 ID AA82615 standard; Protein; 239 AA.

XX AC AA82615;

DT 02-AUG-2000 (first entry)

DE Human PTHrP monoclonal antibody clone 1C1-3 protein SEQ ID NO:14.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 155 /note= "possible Ala"

XX JP2000080100-A.

XX 21-MAR-2000.

XX 12-OCT-1998; 98JP-0304793.

XX 17-JUN-1998; 98JP-0188196.

XX 26-JUN-1998; 98JP-0196729.

XX (NISB) JAPAN TOBACCO INC.

XX WPI; 2000-286723/25.

DR N-PSDB; AAA13925.

XX A human monoclonal antibody to parathyroid hormone related protein. -
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain

PS Claim 31; Page 45-46; 88pp; Japanese.
 XX The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone protein sequence from the
 CC present invention.

XX SQ Sequence 239 AA;

Query Match 87.2%; Score 1083; DB 21; Length 239;
 Best Local Similarity 87.4%; Pred. No. 1.1e-59;
 Matches 209; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSPLPAQLLGLLLCVSGSGEVMTQSPSLPTTPGPASISCRSSQSLKHSNGDTFLSW 60

DB 1 MRLPAQLLGLLMLVPGSGDVMTQSPSLPTTPGPASISCRSSQSLHSGNNYLDW 60

QY 61 YQKPGOPPRLLIYKSNRDSGVDPDRFSGSGAGTDFTLKISAVEAEDVGVFSGGQTRTP 120

DB 61 YLQKPGQPKLLIYKSNRDSGVDPDRFSGSGAGTDFTLKISAVEAEDVGVIYCHQALQTP 120

QY 121 PTGGGQTKVEIKRTVAAPSFIIPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQ 180

DB 121 PTFGPGIKVDIKRTVAAPSFIIPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQ 180

QY 181 SGNSQSVTEQDSKDYSLSSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

DB 181 SGNSQSVTEQDSKDYSLSSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 13

AA82611
 ID AA82611 standard; Protein; 239 AA.

XX AC AA82611;

DT 02-AUG-2000 (first entry)

DE Human PTHrP monoclonal antibody clone 16E12-6 protein SEQ ID NO:6.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

XX Homo sapiens.

XX JP2000080100-A.

XX 21-MAR-2000.

XX 12-OCT-1998; 98JP-0304793.

XX 17-JUN-1998; 98JP-0188196.

XX 26-JUN-1998; 98JP-0196729.

XX (NISB) JAPAN TOBACCO INC.

XX WPI; 2000-286723/25.

DR N-PSDB; AAA13921.

XX A human monoclonal antibody to parathyroid hormone related protein. -
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone

```
Db 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
|||||
RESULT 10
AAW71876
ID AAW71876 standard; Protein; 239 AA.
XX
AC AAW71876;
XX
DT 18-JAN-1999 (first entry)
XX
DE Anti-human Fas humanised antibody CH11 light chain VL-KY.
XX
KW Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;
KW autoimmune disease; rheumatoid arthritis; therapy; human;
KW antibody engineering.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Peptide 1..20
FT /label= Sig_peptide
FT Protein 21..239
FT /label= Mat_protein
FT Region 44..59
FT /label= CDR1
FT /note= "complementarity determining region 1 from
FT CH11 light chain"
FT
FT Region 75..81
FT /label= CDR2
FT /note= "complementarity determining region 2 from
FT CH11 light chain"
FT
FT Region 114..122
FT /label= CDR3
FT /note= "complementarity determining region 3 from
FT CH11 light chain"
FT
XX EP866131-A2.
XX
XX 23-SEP-1998.
XX
XX 20-MAR-1998; 98EP-0302113.
XX
XX 21-MAR-1997; 97JP-0067938.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX Haruyama H, Nakahara K, Serizawa N, Takahashi T;
XX Yonehara S;
XX
XX WPI; 1998-482965/42.
XX N-PSDB; AAV61359.
XX
XX Production of anti-Fas protein humanised antibodies - for use in
XX inducing apoptosis on Fas expressing cells in the treatment of
XX autoimmune diseases, especially rheumatoid arthritis
XX
XX Claim 21; Page 94; 187pp; English.
XX
XX This is the amino acid sequence of a humanised anti-Fas antibody
XX CH11 light chain, designated VL-KY. VL-KY is based on the light
XX chain (see AAW71889) of murine anti-human Fas monoclonal antibody
XX CH11. The humanised sequence was designed following selection of
XX donor residues from CH11 to be grafted onto acceptor molecule
XX RPM16410/Ch. 4 light chain sequences (see AAW71876-79) have been
XX designed, and each can be used in combination with either of 2
XX heavy chain sequences (see AAW71880-81) to provide novel, claimed
XX humanised CH11 IgM antibodies that lack a J chain. These humanised
XX anti-human Fas antibodies are capable of inducing apoptosis in cells
XX expressing Fas (e.g. synovocytes) and are useful in the treatment
XX of autoimmune disease and chronic rheumatoid arthritis. DNA
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CC sequences encoding the humanised antibodies are claimed, as are
CC vectors such as pKkappaK2-58 including the VL-KY nucleotide
CC sequence (see AAV61359), and host cells such as Escherichia coli
CC pKkappaK2-58 (FERM BP-5861).
XX
XX SQ Sequence 239 AA;
XX
XX Query Match 89.4%; Score 1110; DB 19; Length 239;
XX Best Local Similarity 89.5%; Pred. No. 2.4e-61;
XX Matches 214; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
XX
QY 1 MSIPAOQLGLLLCLVCGSSGEVMTQSPSLPTPGCEPASISCRSSQSLKHSNGDTPLSW 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 MRIPAOQLGLLLMLVPGSSGDVMTQSPSLPTLGPASISCRSSKSLVHSGNTYLHW 60
QY 61 YQKPGQPPRLIIYKVNRRDGVDPDFSGSGAGTDFTLKISAVEAEDVGYYFCGQGRTP 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 YLQKPGQSPKLLIYKVNRFSGVDPDFSGSGSGTDFTLKISRVEAEDVGYYCSQSTHVP 120
QY 121 PTFGGTKVRIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQ 180
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 PAFGGTKVRIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQ 180
QY 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 11
AAB12913
ID AAB12913 standard; Protein; 239 AA.
XX
XX AAB12913;
XX
DT 16-NOV-2000 (first entry)
XX
DE Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #78.
XX
XX Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
XX immunosuppression; autoimmune disease; treatment; rheumatism;
XX anti-Fas antibody.
XX
XX Synthetic.
XX
XX JP2000154149-A.
XX
XX 06-JUN-2000.
XX
XX 17-SEP-1999; 99JP-0263984.
XX
XX 18-SEP-1998; 98JP-0264598.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX WPI; 2000-454476/40.
XX N-PSDB; AAA78267.
XX
XX Anti-human Fas humanizing antibody-containing antirheumatic agents -
XX Claim 1; Page 66-67; 109pp; Japanese.
XX
XX The present invention relates to antirheumatic agents which comprise as
XX active ingredients an immunoglobulin M (IgM) protein. The IgM protein
XX does not include a J segment, has apoptosis inducing activity, and
XX consists of a light and heavy chain polypeptide produced synthetically.
XX The agents of the invention exhibit antirheumatic and immunosuppressive
XX activity and can be used to treat autoimmune diseases, especially
XX rheumatism. The IgM molecule used in the invention has human Fas-antigen
XX binding properties. Included in the invention are nucleotide sequences
XX of the IgM light and heavy chains (see AAB12913-B12918 and AAB12919), and
XX corresponding protein sequences (see AAB12913-B12918 and AAB12919), and
XX nucleotide sequences of the humanised anti-human Fas Ig Ch11 (see
XX AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also
```


XX Claim 23; Page 96-97; 187pp; English.

PS This is the amino acid sequence of a humanised anti-Fas antibody

XX CH11 light chain, designated VL-KF. VL-KF is based on the light

CC chain (See AAW71899) of murine anti-human Fas monoclonal antibody

CC CH11. The humanised sequence was designed following selection of

CC donor residues from CH11 to be grafted onto acceptor molecule

CC RPM16410/CL. 4 Light chain sequences (see AAW71876-79) have been

CC designed, and each can be used in combination with either of 2

CC heavy chain sequences (see AAW71880-81) to provide novel, claimed

CC humanised CH11 IGM antibodies that lack a J chain. These humanised

CC anti-human Fas antibodies are capable of inducing apoptosis in cells

CC expressing Fas (e.g. synovocytes) and are useful in the treatment

CC of autoimmune disease and chronic rheumatoid arthritis. DNA

CC sequences encoding the humanised antibodies are claimed, as are

CC vectors such as pKappaK2-19 including the VL-KF nucleotide

CC sequence (see AAV61360) and host cells such as Escherichia coli

CC pKappaK2-19 (FERM BP-5860).

XX Sequence 239 AA;

Query Match 89.6%; Score 1113; DB 19; Length 239;

Best Local Similarity 90.0%; Pred. No. 1.6e-61;

Matches 215; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLCVPGSSGVVMTQPSLPTGEPASISCRSSQSLKHSNGDTFLSW 60

DB 1 MRLPAQLGLLLMLWVPGSSGDDVMTQPSLPTLGQPASISCRSSKSLVHSGNTYLHW 60

QY 61 YQKPGQPPRLIIYKVNRSRSGVDPDRFGSGGAGTDTLTKISAVEAEDVGVYFCQGTTRP 120

DB 61 YLQKPGQPKLLIYKVNRSRSGVDPDRFGSGSGGTDFTLKISRVEAEDVGVYFCSQSTHP 120

QY 121 PTFGGGTKEIKRTVAAPSVEIFPPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180

DB 121 PAFGGGTKEIKRTVAAPSVEIFPPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180

QY 181 SGNQSVTEQDSKDYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 239

DB 181 SGNQSVTEQDSKDYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 239

RESULT 7

AAW71878

ID AAW71878 standard; Protein; 239 AA.

AC AAW71878;

XX

DT 18-JAN-1999 (first entry)

XX

DE Anti-human Fas humanised antibody CH11 light chain VL-RY.

XX

KW Humanised antibody; Fas; CH11; monoclonal antibody; MAB; apoptosis;

KW autoimmune disease; rheumatoid arthritis; therapy; human;

KW antibody engineering.

XX

OS Homo sapiens.

OS Synthetic.

XX

PH Key Location/Qualifiers

FT Peptide 1..20

FT Peptide 21..239

FT Protein 44..59

FT Region 44..59

FT /label= CDR1

FT /note= "complementarity determining region 1 from

FT CH11 light chain"

FT

FT Region 75..81

FT /label= CDR2

FT /note= "complementarity determining region 2 from

FT CH11 light chain"

FT

FT Region 114..122

PS /label= CDR3

XX /note= "complementarity determining region 3 from

XX CH11 light chain"

PN EP866131-A2.

XX 23-SEP-1998.

PD

XX 20-MAR-1998; 98EP-0302113.

PF

XX 21-MAR-1997; 97JP-0067938.

PR

XX (SANY) SANKYO CO LTD.

PA Haruyama H, Nakahara K, Serizawa N, Takahashi T;

PI Yonehara S;

XX WPI: 1998-482965/42.

DR N-PSDB; AAV61362.

XX Production of anti-Fas protein humanised antibodies - for use in

PT inducing apoptosis on Fas expressing cells in the treatment of

PT autoimmune diseases, especially rheumatoid arthritis

XX Claim 25; Page 99; 187pp; English.

XX This is the amino acid sequence of a humanised anti-Fas antibody

CC CH11 light chain, designated VL-RY. VL-RY is based on the light

CC chain (see AAW71889) of murine anti-human Fas monoclonal antibody

CC CH11. The humanised sequence was designed following selection of

CC donor residues from CH11 to be grafted onto acceptor molecule

CC RPM16410/CL. 4 Light chain sequences (see AAW71876-79) have been

CC designed, and each can be used in combination with either of 2

CC heavy chain sequences (see AAW71880-81) to provide novel, claimed

CC humanised CH11 IGM antibodies that lack a J chain. These humanised

CC anti-human Fas antibodies are capable of inducing apoptosis in cells

CC expressing Fas (e.g. synovocytes) and are useful in the treatment

CC of autoimmune disease and chronic rheumatoid arthritis. DNA

CC sequences encoding the humanised antibodies are claimed, as are

CC vectors such as pKappaRY2-10 including the VL-RY nucleotide

CC sequence (see AAV61361), and host cells such as Escherichia coli

CC pKappaRY2-10 (FERM BP-5859).

XX Sequence 239 AA;

Query Match 89.6%; Score 1113; DB 19; Length 239;

Best Local Similarity 90.0%; Pred. No. 1.6e-61;

Matches 215; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLCVPGSSGVVMTQPSLPTGEPASISCRSSQSLKHSNGDTFLSW 60

DB 1 MRLPAQLGLLLMLWVPGSSGDDVMTQPSLPTLGQPASISCRSSKSLVHSGNTYLHW 60

QY 61 YQKPGQPPRLIIYKVNRSRSGVDPDRFGSGGAGTDTLTKISAVEAEDVGVYFCQGTTRP 120

DB 61 YLQKPGQPKLLIYKVNRSRSGVDPDRFGSGSGGTDFTLKISRVEAEDVGVYFCSQSTHP 120

QY 121 PTFGGGTKEIKRTVAAPSVEIFPPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180

DB 121 PAFGGGTKEIKRTVAAPSVEIFPPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180

QY 181 SGNQSVTEQDSKDYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 239

DB 181 SGNQSVTEQDSKDYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 239

RESULT 8

AAW712914

ID AAW712914 standard; Protein; 239 AA.

XX

AC AAW712914;

XX

QY 61 YQKPGQPRLLIYKVNRSQGVDPDRFSGSGAGTDTLTKISAVEAEDVGVFCGGTTRTP 120
 DB 61 YLQKPGQPRLLIYKVNRSQGVDPDRFSGSGAGTDTLTKISAVEAEDVGVFCGGTTRTP 120
 QY 121 PTCGGTKEIKRTVAASVFIIPPDSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180
 DB 121 PARQGGTKEIKRTVAASVFIIPPDSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180
 QY 181 SGNQSQSVTEQSDKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTXSNRGE 239
 DB 181 SGNQSQSVTEQSDKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTXSNRGE 239

RESULT 5
 AAB12916
 ID AAB12916 standard; Protein; 239 AA.
 XX
 AC AAB12916;
 DT 16-NOV-2000 (first entry)
 DE Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #84.
 DE Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
 KW immunosuppression; autoimmune disease; treatment; rheumatism;
 KW anti-Fas antibody.
 XX
 OS Synthetic.
 XX
 PN JP2000154149-A.
 XX
 PD 06-JUN-2000.
 XX
 PF 17-SEP-1999; 99JP-0263984.
 XX
 PR 18-SEP-1998; 98JP-0264598.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI; 2000-454476/40.
 DR N-PSDB; AAA78270.
 XX
 PT Anti-human Fas humanizing antibody-containing antirheumatic agents -
 XX
 PS Claim 1; Page 72-73; 109pp; Japanese.
 CC The present invention relates to antirheumatic agents which comprise as
 CC active ingredient an immunoglobulin M (IgM) protein. The IgM protein
 CC does not include a J segment, has apoptosis inducing activity and
 CC consists of a light and heavy chain polypeptide produced synthetically.
 CC The agents of the invention exhibit antirheumatic and immunosuppressive
 CC activity and can be used to treat autoimmune diseases, especially
 CC rheumatism. The IgM molecule used in the invention has human Fas-antigen
 CC binding properties. Included in the invention are nucleotide sequences
 CC of the IgM light and heavy chains (see AAB78267-A78272) and the
 CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and
 CC nucleotide sequences of the humanised anti-human Fas Ig ChII (see
 CC AAB78202-A78206) and protein sequences (see AAB12908-B12910). Also
 CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).
 CC Primers specific for the anti-human Fas antibody, light, heavy and kappa
 CC chains used in the invention are represented by sequences
 CC AAB78213-A78266. Primers used for sequencing the human Ig DNA used in the
 CC invention are represented by sequences AAB78277-A78318 and
 CC AAB78335-A78337, while humanised anti-Fas Ig DNA sequencing primers are
 CC represented by sequences AAB78321-A78334 and AAB78338-A78367. Primer
 CC sequences AAB78207-A78212 are specific for murine Ig DNA, and are used in
 CC the production of the agent of the invention.
 XX
 SQ Sequence 239 AA;
 Query Match 89.9%; Score 1116; DB 21; Length 239;
 Best Local Similarity 90.4%; Prd. No. 1e-61;

Matches 216; Conservative 8; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MSYPAQLGLLLCVPGSSGEVMTQSPSLSPITPGEPASISCRSSQSLCHSNGDTLSW 60
 DB 1 YLQKPGQPRLLIYKVNRSQGVDPDRFSGSGAGTDTLTKISAVEAEDVGVFCGGTTRTP 120
 QY 61 YQKPGQPRLLIYKVNRSQGVDPDRFSGSGAGTDTLTKISAVEAEDVGVFCGGTTRTP 120
 DB 61 YLQKPGQPRLLIYKVNRSQGVDPDRFSGSGAGTDTLTKISAVEAEDVGVFCGGTTRTP 120
 QY 121 PTCGGTKEIKRTVAASVFIIPPDSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180
 DB 121 PARQGGTKEIKRTVAASVFIIPPDSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180
 QY 181 SGNQSQSVTEQSDKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTXSNRGE 239
 DB 181 SGNQSQSVTEQSDKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTXSNRGE 239

RESULT 6
 AAW71877
 ID AAW71877 standard; Protein; 239 AA.
 XX
 AC AAW71877;
 DT 18-JAN-1999 (first entry)
 DE Anti-human Fas humanised antibody CH11 light chain VL-KF.
 DE Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;
 KW autoimmune disease; rheumatoid arthritis; therapy; human;
 KW antibody engineering.
 XX
 OS Homo sapiens.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Peptide
 FT /label= Sig_peptide
 FT 21..239
 FT /label= Mat_protein
 FT 44..59
 FT /label= CDR1
 FT /note= "complementarity determining region 1 from
 FT CH11 light chain"
 FT Region
 FT 75..81
 FT /label= CDR2
 FT /note= "complementarity determining region 2 from
 FT CH11 light chain"
 FT Region
 FT 114..122
 FT /label= CDR3
 FT /note= "complementarity determining region 3 from
 FT CH11 light chain"
 XX
 PN EP866131-A2.
 XX
 PD 23-SEP-1998.
 XX
 PF 20-MAR-1998; 98EP-0302113.
 XX
 PR 21-MAR-1997; 97JP-0067938.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 XX Haruyama H, Nakahara K, Serizawa N, Takahashi T;
 PI Yonehara S;
 XX WPI; 1998-482965/42.
 DR N-PSDB; AAV61360.
 XX
 PT Production of anti-Fas protein humanised antibodies - for use in
 PT inducing apoptosis on Fas expressing cells in the treatment of
 PT autoimmune diseases, especially rheumatoid arthritis

XX PD 29-NOV-2001.
 XX PF 22-MAY-2001; 2001WO-US16364.
 XX PR 22-MAY-2000; 2000US-0576424.
 XX PA (IDEC-) IDEC PHARM CORP.
 XX PI Anderson DR, Hanna N, Brama P;
 XX PR WPI; 2002-089895/12.
 XX DR N-PSDB; AAS17244.
 XX PT Use of monoclonal antibody which specifically binds to B7.1 antigen
 FT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
 FT treating cancer, graft-vs-host disease and autoimmune disease such as
 FT allergy -
 XX PS Example 8; Fig 4a; 89pp; English.
 XX CC The present invention relates to a new use of a monoclonal antibody
 CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
 CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
 CC useful for treating diseases such as B cell cancer, lymphoma, a
 CC cancer where B cells promote the growth and/or metastasis of tumours,
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosis,
 CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
 CC or graft-vs-host disease. The antibody is useful for immunosuppression
 CC in a human or animal and for treating or preventing resistance to or
 CC rejection of transplanted organ or tissue for treating proliferative
 CC and hyperproliferative diseases, for treating reversible obstructive
 CC airways disease, intestinal inflammations and allergies e.g. Crohn's
 CC disease and ulcerative colitis, food-related allergies e.g. migraine,
 CC rhinitis and eczema, and other types of allergies. The present protein
 CC sequence represents the light chain of 786, a primatised antibody
 CC used in the invention to induce apoptosis.
 XX SQ Sequence 239 AA;

Query Match 100.0%; Score 1242; DB 23; Length 239;
 Best Local Similarity 100.0%; Pred. No. 1.7e-69;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSLPAQLGLLLLCVPGSGEVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
 Db 1 MSLPAQLGLLLLCVPGSGEVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
 Qy 61 YQKPGQPRLIIYKVNRSNDSGVPDRFSGSGAGTDTLTKISAVEAEDGVVFCQGRTRP 120
 Db 61 YQKPGQPRLIIYKVNRSNDSGVPDRFSGSGAGTDTLTKISAVEAEDGVVFCQGRTRP 120
 Qy 121 PTFGGGTVEIKRTVAAPSVEFPSPDSQSLKSGTASVVCLLNFFPREAKVQWKNALQ 180
 Db 121 PTFGGGTVEIKRTVAAPSVEFPSPDSQSLKSGTASVVCLLNFFPREAKVQWKNALQ 180
 Qy 181 SGNQSEVTEODSKDSTYLSSTLTSLKADYKHKVACEVTHQGLSPVTKSENREGC 239
 Db 181 SGNQSEVTEODSKDSTYLSSTLTSLKADYKHKVACEVTHQGLSPVTKSENREGC 239

RESULT 4
 AA71879
 ID AA71879 standard; Protein; 239 AA.
 XX AC AA71879;
 XX DT 18-JAN-1999 (first entry)

XX DB Anti-human Fas humanised antibody CH11 light chain VL-RF.

KW Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;
 KW autoimmune disease; rheumatoid arthritis; therapy; human;
 KW antibody engineering.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Location/Qualifiers
 FT Key 1..20
 FT Peptide /label= Sig_peptide
 FT Protein 21..239
 FT Region /label= Mat_protein
 FT 44..59
 FT 1..59 CDR1
 FT /label= CDR1
 FT /notes= "complementarity determining region 1 from
 FT CH11 light chain"
 FT Region 75..81
 FT /label= CDR2
 FT /notes= "complementarity determining region 2 from
 FT CH11 light chain"
 FT Region 114..122
 FT /label= CDR3
 FT /notes= "complementarity determining region 3 from
 FT CH11 light chain"
 XX EP866131-A2.
 XX 23-SEP-1998.
 XX 20-MAR-1998; 98EP-0302113.
 XX 21-MAR-1997; 97JP-0067938.
 XX (SANY) SANKYO CO LTD.
 XX Hanyama H, Nakahara K, Serizawa N, Takahashi T;
 XX Itohara S;
 XX WPI; 1998-482965/42.
 XX N-PSDB; AAV61362.
 XX Production of anti-Fas protein humanised antibodies - for use in
 XX inducing apoptosis on Fas expressing cells in the treatment of
 XX autoimmune diseases, especially rheumatoid arthritis
 XX Claim 27; Page 101-102; 187pp; English.
 XX This is the amino acid sequence of a humanised anti-Fas antibody
 XX CH11 light chain, designated VL-RF. VL-RF is based on the light
 XX chain (see AAW71889) of murine anti-human Fas monoclonal antibody
 XX CH11. The humanised sequence was designed following selection of
 XX donor residues from CH11 to be grafted onto acceptor molecule
 XX RPI6410'CL. 4 Light chain sequences (see AAW71876-79) have been
 XX designed, and each can be used in combination with either of 2
 XX heavy chain sequences (see AAW71880-81) to provide novel, claimed
 XX humanised CH11 IGM antibodies that lack a J chain. These humanised
 XX anti-human Fas antibodies are capable of inducing apoptosis in cells
 XX expressing Fas (e.g. synovocytes) and are useful in the treatment
 XX of autoimmune disease and chronic rheumatoid arthritis. DNA
 XX sequences encoding the humanised antibodies are claimed, as are
 XX vectors such as pKappARF2-52 including the VL-RF nucleotide
 XX sequence (see AAV61362), and host cells such as Escherichia coli
 XX pKappARF2-52 (FERM BP-5862).
 XX SQ Sequence 239 AA;
 Query Match 89.9%; Score 1116; DB 19; Length 239;
 Best Local Similarity 90.4%; Pred. No. 1e-61;
 Matches 216; Conservative 8; Mismatches 15; Indels 0; Gaps 0;
 Qy 1 MSLPAQLGLLLLCVPGSGEVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
 Db 1 MSLPAQLGLLLLCVPGSGEVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60

DR N-PSDB; AAT62511.
 XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
 PT useful for treating autoimmune disease or graft-versus-host disease
 PT
 PS Claim 8; Fig 9A; 81pp; English.
 XX
 CC 2 Polypeptides (AAW01819 and AAW01820) respectively comprise primatised
 CC forms of the light and heavy chains of cynomolgus monkey anti-human
 CC B7.1 antigen monoclonal antibody 7B6. Cloned 7B6 light and heavy
 CC variable genes (see also AAT62511 and AAT13847) are inserted into
 CC an expression vector (pref. NEOSPLA) which contains human light and
 CC heavy chain constant region genes to allow prodn. of the primatised
 CC antibody in e.g. CHO cells. Primatised 7C10 and 16C10 anti-B7.1
 CC antibodies have also been produced (see also AAW01817-19 and
 CC AAW01821-22). The primatised antibodies inhibit the B7:CD28 pathway,
 CC making them useful immunosuppressants for the treatment of
 CC autoimmune disorders and graft-versus-host disease.
 XX
 SQ Sequence 239 AA;
 Query Match 100.0%; Score 1242; DB 18; Length 239;
 Best Local Similarity 100.0%; Pred. No. 1.7e-69;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLPAQLGLLLCVPGSGGEVMTQSPSLPTITGEPASISCRSSQSLKHNGDTFLSW 60
 DB 1 MSLPAQLGLLLCVPGSGGEVMTQSPSLPTITGEPASISCRSSQSLKHNGDTFLSW 60
 QY 61 YQKPGOPRLIYKVNRDGVDPFSGSGAGDTFTLKISAVEAEVGVYFCGGQTRTP 120
 DB 61 YQKPGOPRLIYKVNRDGVDPFSGSGAGDTFTLKISAVEAEVGVYFCGGQTRTP 120
 QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQ 180
 DB 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQ 180
 QY 181 SGNQSESVTEQDSKSTVSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239
 DB 181 SGNQSESVTEQDSKSTVSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239
 RESULT 2
 AAW63762
 ID AAW63762 standard; Protein; 239 AA.
 AC AAW63762;
 XX
 XX 29-SEP-1998 (first entry)
 DT
 DE Macaque primatised 7B6 light chain protein.
 XX
 KW Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
 KW immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
 XX T cell proliferation.
 XX
 OS Macaca fascicularis.
 XX
 PN WO9819706-A1.
 XX
 PD 14-MAY-1998.
 XX
 PF 29-OCT-1997; 97WO-US19906.
 XX
 PR 08-NOV-1996; 96US-0746361.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Anderson DR, Brans P, Hanna N;
 XX
 XX WPI; 1998-286f01/25.

DR N-PSDB; AAV35486.
 XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 PT inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 PT cells, e.g. graft rejection or tumours
 XX
 PS Example 7; Fig 4a; 87pp; English.
 XX
 CC This sequence represents a primatised form of the antibody 7B6 light
 CC chain from macaque. This sequence is used in a method which studies new
 CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC Mab's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 CC host diseases, B cell lymphoma, infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop
 CC anti-idiotype reagents. Mab's are optionally combined with other proteins
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.
 XX
 SQ Sequence 239 AA;
 Query Match 100.0%; Score 1242; DB 19; Length 239;
 Best Local Similarity 100.0%; Pred. No. 1.7e-69;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLPAQLGLLLCVPGSGGEVMTQSPSLPTITGEPASISCRSSQSLKHNGDTFLSW 60
 DB 1 MSLPAQLGLLLCVPGSGGEVMTQSPSLPTITGEPASISCRSSQSLKHNGDTFLSW 60
 QY 61 YQKPGOPRLIYKVNRDGVDPFSGSGAGDTFTLKISAVEAEVGVYFCGGQTRTP 120
 DB 61 YQKPGOPRLIYKVNRDGVDPFSGSGAGDTFTLKISAVEAEVGVYFCGGQTRTP 120
 QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQ 180
 DB 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQ 180
 QY 181 SGNQSESVTEQDSKSTVSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239
 DB 181 SGNQSESVTEQDSKSTVSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239
 RESULT 3
 AAV1540
 ID AAV1540 standard; Protein; 239 AA.
 XX
 AC AAV1540;
 XX
 XX 12-MAR-2002 (first entry)
 DT
 DE
 DE Protein sequence of primatised form of the light chain of 7B6 antibody.
 XX
 KW Human; macaque monkey; light chain; primatised antibody; 7B6 antibody;
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
 KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
 KW graft-vs-host disease; immunosuppression; organ rejection;
 KW interleukin-2; IL-2; mutant; mutein.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Macaca sp.
 XX Synthetic.
 XX
 PN WO200189567-A1.

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 24.5816 Seconds
(without alignments)
1295.559 Million cell updates/sec

Title: US-09-758-173-6

Perfect score: 1242

Sequence: 1 MSLPAQLGLLLCVPGSSG.....EVTHQLSSPVTXSFNRGFC 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1242	100.0	239	18	AAW01819
2	1242	100.0	239	19	AAW53762
3	1242	100.0	239	23	AAU11540
4	1116	89.9	239	19	AAW71879
5	1116	89.9	239	21	AAAB12916
6	1113	89.6	239	19	AAW71877
7	1113	89.6	239	19	AAW71878
8	1113	89.6	239	21	AAAB12914
9	1113	89.6	239	21	AAAB12915
10	1110	89.4	239	19	AAW71876

11	1110	89.4	239	21	AAAB12913
12	1083	87.2	239	21	AAAY82615
13	1065	85.7	239	21	AAAY82611
14	1063	85.6	239	21	AAAY82610
15	1063	85.6	239	21	AAAY82617
16	1061	85.4	239	21	AAAY82614
17	1057	85.1	239	21	AAAY82616
18	1052.5	84.7	238	18	AAW14942
19	1052.5	84.7	238	18	AAW14937
20	1050	84.5	239	21	AAAY82613
21	1044	84.1	239	21	AAAY82612
22	1042	83.9	241	21	AAAY96303
23	1038.5	83.6	238	22	AAU07744
24	1037.5	83.5	238	17	AAAR93554
25	1032	82.3	239	21	AAU77298
26	1018	82.0	239	21	AAAY82618
27	1016	81.8	239	21	AAAY82619
28	1007	81.1	238	22	AAAB72227
29	1007	81.1	238	22	AAAB72231
30	1007	81.1	238	22	AAAB72233
31	1007	81.1	238	22	AAAB72235
32	992.5	79.9	220	22	AAE12714
33	978	78.7	241	13	AAAR28809
34	976.5	78.6	238	19	AAW83034
35	976.5	78.6	238	21	AAAB14777
36	976.5	78.6	238	21	AAW90927
37	976.5	78.6	238	23	AAAB74896
38	976.5	78.6	238	23	AAAB74942
39	976	78.6	242	16	AAAR86323
40	976	78.6	242	18	AAW42323
41	976	78.6	242	18	AAW31580
42	976	78.6	242	18	AAW23790
43	976	78.6	242	19	AAW69311
44	976	78.6	242	19	AAW40126
45	976	78.6	242	19	AAW33745

ALIGNMENTS

RESULT 1
AAW01819
ID AAW01819 standard; Protein; 239 AA.
XX AC AAW01819;
XX DT 25-MAY-1997 (first entry)
XX DE Primatised anti-human B7.1 antigen antibody 7B6 light chain.
XX KW Monoclonal antibody; cynomolgus monkey; macaque; 7B6;
XX KW Primatised antibody; B7 antigen; CD28; immunosuppressive;
XX KW autoimmune disease; idiopathic thrombocytopenia purpura;
XX KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
XX KW type 1 diabetes mellitus; graft versus host disease;
XX KW hetero-hybridoma; transfectoma.
XX OS Chimeric Macaca cynomolgus;
XX OS Chimeric Homo sapiens.
XX PN WO9640878-A1.
XX PD 19-DEC-1996.
XX PF 06-JUN-1996; 96WO-US10053.
XX PR 07-JUN-1995; 95US-0487550.
XX PA (IDEC-) IDEC PHARM CORP.
XX PI Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX WP1; 1997-108638/10.

Hypothetical 24.9 kDa protein.
DE Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020298; AAH2098.1; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; Ig_2.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_1.
SQ SEQUENCE 237 AA; 24884 MW; E6CF371E753968E8 CRC64;

Query Match 35.2%; Score 437.5; DB 4; Length 237;
Best Local Similarity 42.4%; Pred. No. 3.6e-33;
Matches 101; Conservative 44; Mismatches 80; Indels 13; Gaps 8;
QY 7 LIGLLLCVPGSGEVMTQSPLSLPTPGEPAISICRSQSLKHSNGDTFLSWYQQKPG 66
Db 7 LUTLLAHT-GSWAQSVLTQPP-SVSGAPQQRVTISCTGSSSNIGAGYD--VHWYQQLPG 62
QY 67 QPRLIYKVSNRDGVDPDRFSGSGAGTDTLTKISAVEAEDVGVFYFCGQTRTPPTF 123
Db 63 TAPKLLIYGNRNPSGVDPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDLSASGVF 122
QY 124 GGGTKVEI-KRTVAAPSVFIFPPSDEQLKSGTASVCLLNFPYREAKVQWKVDNA-LQS 181
Db 123 GGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKA 182
QY 182 GNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 239
Db 183 G--VETTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEG--STVEKTVAPTEC 236

RESULT 15
Q8WUK4 PRELIMINARY; PRT; 237 AA.
AC Q8WUK4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 24.9 kDa protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020233; AAH20233.1; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; Ig_2.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_1.
SQ SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;

Query Match 35.0%; Score 434.5; DB 4; Length 237;
Best Local Similarity 42.4%; Pred. No. 6.9e-33;
Matches 101; Conservative 45; Mismatches 79; Indels 13; Gaps 8;
QY 7 LIGLLLCVPGSGEVMTQSPLSLPTPGEPAISICRSQSLKHSNGDTFLSWYQQKPG 66
Db 7 LUTLLAHT-GSWAQSVLTQPP-SVSGAPQQRVTISCTGSSSNIGAGYD--VHWYQQLPG 62
QY 67 QPRLIYKVSNRDGVDPDRFSGSGAGTDTLTKISAVEAEDVGVFYFCGQTRTPPTF 123
Db 63 TAPKLLIYGNRNPSGVDPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDLSGFWVF 122
QY 124 GGGTKVEI-KRTVAAPSVFIFPPSDEQLKSGTASVCLLNFPYREAKVQWKVDNA-LQS 181
Db 123 GGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKA 182
QY 182 GNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 239
Db 183 G--VETTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEG--STVEKTVAPTEC 236

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Job time : 22.6765 secs

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003600; Ig like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 214
FT SEQUENCE 214 AA; 23922 MW; 52BA205FDE9595E2A CRC64;
Query Match 51.4%; Score 638.5; DB 11; Length 214;
Best Local Similarity 53.9%; Pred. No. 3.7e-52;
Matches 118; Conservative 42; Mismatches 54; Indels 5; Gaps 1;
QY 21 EVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRD 80
DB 1 DIQUTQSPSSWASLGERVITTCASQDI-----NSVLSWFQKPKSPKTLIYRANRLV 55
QY 81 SGVDPDRFSGSGAGTDFTLKISAVEAEADVGVYFCQGQTRTPP-TFGGGTKVEIKR 140
DB 56 DGVPSRFSGSGGQDYSLTISSLEYEDMWGYICLYQDEFPTFGSGTKLEIKRAADAFTV 115
QY 141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQGNLSQVSEVTEQDSKDSTYSL 200
DB 116 SIFPPSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 175
QY 201 SSTLTLSKADYEKHKVACETVTHOGLSPVTKSFNRGEC 239
DB 176 SSTLTLDKDEYERNSTCEATHKTSPIVKCFNRNEC 214
RESULT 12
Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035034; AAD56270.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1
FT NON_TER 114
FT SEQUENCE 114 AA; 12775 MW; 070B31E210D1CB01 CRC64;
Query Match 37.2%; Score 462.5; DB 4; Length 114;
Best Local Similarity 78.9%; Pred. No. 5.7e-36;
Matches 90; Conservative 12; Mismatches 11; Indels 1; Gaps 1;
QY 21 EVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRD 80
DB 1 DVVMTQSPSLPVLTRQPAISCRSSQSPVYSDGNTLNNWFQQRPQSPRRLIIYKVSNRD 60
QY 81 SGVDPDRFSGSGAGTDFTLKISAVEAEADVGVYFCQGQTRTPP-TFGGGTKVEIKR 133
DB 61 SGVDPDRFSGSGGTDFTLKISRVEAEDVGVYCMQGTHTPWTFTGGTKVEIKR 114
RESULT 13
Q8TEC9 PRELIMINARY; PRT; 233 AA.
AC Q8TEC9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 24.9 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS;
RA Strausberg R.;
RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022823; AAH22823.1; -.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;
Query Match 37.1%; Score 460.5; DB 4; Length 233;
Best Local Similarity 42.7%; Pred. No. 2.4e-35;
Matches 103; Conservative 45; Mismatches 70; Indels 23; Gaps 9;
QY 7 LLGLLLLCVPGSSGEVMTQSPSLPITPGEPASISCRSSQSLKHSNGDT---FLSWYQ 62
DB 7 LLPLTLCT-GSEASVELTQPP-SVSVSPGQTARITC-----SGDALPKQYAYWYQ 55
QY 63 QKPGQPPRLIIYKVSNRDGVDPDRFSGSGAGTDFTLKISAVEAEADVGVYFC--GGGTETP 120
DB 56 QKPGQAPVLVIYKDNERPSPGIPERFSGSSSGTFTVLTITSGVQAEDEADYYCOSADSSGT 115
QY 121 PTFGGTKVEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA- 178
DB 116 WYFGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSP 175
QY 179 LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGE 238
DB 176 VKAG--VETTTSPKSNKNKYAASSVLSLTPEQWKSHKSYSCQVTHEG--STVEKTVAPTE 231
QY 239 C 239
DB 232 C 232
RESULT 14
Q8WTU6 PRELIMINARY; PRT; 237 AA.
AC Q8WTU6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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QY 181 SGNQSQSVTEQDSKDYSLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 176 QNGVLNSWTDQDSKDYSSSTLTTLTKDEYERHNSYTCEATHKTSTSPVKSFNREC 234

RESULT 8
Q91W12
ID Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD583FEF CRC64;

Query Match
Best Local Similarity 53.1%; Score 667; DB 11; Length 235;
Matches 128; Conservative 37; Mismatches 68; Indels 8; Gaps 2;

QY 1 MSIPALLGLLL--CVPSSGEVMTQSLPITPGEPAISICRSSQSLKHSNGDTFL 58
Db 1 MDPQVIFGLLISAVIISRGQVLTQSPAINASPGERVMTCSASSVSH-----M 54

QY 59 SWYQKPGPPRLIIYKVNRSQVDPDRFSGGAGDTFLKISAVEAEDVGVVFCQGTR 118
Db 55 HWYQKSGTSPKEWIDYTFKLTSQVDPDRFSGSGSTSYSLTISNMEAEADVATYQCQWSR 114

QY 119 TPTFGGGTVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPREAKVQKVDNA 178
Db 115 NPPTFGVGTGKLELRADAAPTIVSIFPPSDEQLTSGASVVCFLNNFYPKDINVKWKIDGS 174

QY 179 LOSGNSQSVTEQDSKDYSLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGE 238
Db 175 ERQNGVLNSWTDQDSKDYSSSTLTTLTKDEYERHNSYTCEATHKTSTSPVKSFNRE 234

QY 239 C 239
Db 235 C 235

RESULT 9
Q8R028
ID Q8R028 PRELIMINARY; PRT; 234 AA.
AC Q8R028
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028540; AAH28540.1; -.
KW Hypothetical protein.

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SQ SEQUENCE 234 AA; 25702 MW; 148377F9C1CD0ABE CRC64;

Query Match
Best Local Similarity 52.9%; Score 656.5; DB 11; Length 234;
Matches 128; Conservative 30; Mismatches 72; Indels 5; Gaps 1;

QY 5 AQLGLALLLCVPGSSGEVMTQSLPITPGEPAISICRSSQSLKHSNGDTFLSWYQOK 64
Db 5 APLLSLLLLCVSDSRAETTVTQSPASLSVATGKVTIRCTITSDI-----DDDMNMYQOK 59

QY 65 PGQPPRLIIYKVNRSQVDPDRFSGGAGDTFLKISAVEAEDVGVVFCQGTRTPPTFG 124
Db 60 PGEPPKLLISEGNTLRGVPSPRFSSSGVTGDFVFTIENTLSEADVADYICLQSDNMPITFG 119

QY 125 GGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNS 184
Db 120 AGTKLELRADAAPTIVSIFPPSDEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGV 179

QY 185 QESVTEQDSKDYSLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 180 LNSWTDQDSKDYSSSTLTTLTKDEYERHNSYTCEATHKTSTSPVKSFNREC 234

RESULT 10
Q91WS9
ID Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match
Best Local Similarity 52.8%; Score 655.5; DB 11; Length 233;
Matches 127; Conservative 34; Mismatches 63; Indels 5; Gaps 1;

QY 11 LLLCVPGSSGEVMTQSLPITPGEPAISICRSSQSLKHSNGDTFLSWYQOKPGQPPR 70
Db 10 LLLCFQGSRCDIQMTQTSLSASLGRVITISCSGSGIAN-----VLNMYQKPDGTVK 64

QY 71 LLIVKVNRSQVDPDRFSGGAGDTFLKISAVEAEDVGVVFCQGTRTPPTFGGKTVE 130
Db 65 LLIIYTSLSHSGVPSRPSGSGTGYSLTISNLEPEDIATYCCQYRYLPFTWTFGGTKLE 124

QY 131 IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQSVTE 190
Db 125 IKRADAAPTIVSIFPPSDEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWD 184

QY 191 QDSKDYSLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 185 QDSKDYSLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 233

RESULT 11
Q9RIAS
ID Q9RIAS PRELIMINARY; PRT; 214 AA.
AC Q9RIAS;

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Db 61 YLQKPGSQQLLIYVSNRFGVDPDRFSGSGGTDTFTLKISAVEADLVGYVCFQSNHLP 120
Qy 121 PTFGGGTVKEIKRTVAAPSFIIPPPSDEOLKSGTASVCLLNNEYPREAKVQWKVDNALQ 180
Db 121 YTFGGGTVKEIKRADAAPTVSIIPPPSDEOLKSGTASVCLLNNEYPKDINVKWKIDGSR 180
Qy 181 SGNQSQSVTEQDSKDSYSLSSLTLSKADYKHVKYACVETHQGLSSPVTKSFNRGEC 239
Db 181 QNGVLNSWTDQDSKDSYSSMTLTITKDEYERHNSYTCETHTKTSTSPIVKSFNRNEC 239

RESULT 5
Q8VCP0 PRELIMINARY; PRT; 234 AA.
AC Q8VCP0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP TISSUE=COLON;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019474; AAH19474.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2A9F CRC64;

Query Match 55.7%; Score 691.5; DB 11; Length 234;
Best Local Similarity 54.0%; Pred. No. 4.2e-57;
Matches 129; Conservative 44; Mismatches 61; Indels 5; Gaps 1;

Qy 1 MSLPAQLGLLLLCVPGSSGEVVMVTPGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MSVPTQVLGLLLCLTGARCDIQLTSPASLSASVGETVITCRASENIY-----SYLAW 55

Qy 61 YQKPGQPRLIIYKVNRSQVDPDRFSGSGAGTDTFTLKISAVEADVGVYFCQGTRTP 120
Db 56 YQKQKSPQLLVYNAXTLADGVPSRFSRSGTQSLKINSIQPEDFGSYCYQHHSGIP 115

Qy 121 PTFGGGTVKEIKRTVAAPSFIIPPPSDEOLKSGTASVCLLNNEYPREAKVQWKVDNALQ 180
Db 116 FTFGGGTVKEIKRADAAPTVSIIPPPSDEOLKSGTASVCLLNNEYPKDINVKWKIDGSR 175

Qy 181 SGNQSQSVTEQDSKDSYSLSSLTLSKADYKHVKYACVETHQGLSSPVTKSFNRGEC 239
Db 181 QNGVLNSWTDQDSKDSYSSMTLTITKDEYERHNSYTCETHTKTSTSPIVKSFNRNEC 234

Query Match 55.7%; Score 691.5; DB 11; Length 234;
Best Local Similarity 54.0%; Pred. No. 4.2e-57;
Matches 129; Conservative 44; Mismatches 61; Indels 5; Gaps 1;

Qy 1 MSLPAQLGLLLLCVPGSSGEVVMVTPGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MSVPTQVLGLLLCLTGARCDIQLTSPASLSASVGETVITCRASENIY-----SYLAW 55

Qy 61 YQKPGQPRLIIYKVNRSQVDPDRFSGSGAGTDTFTLKISAVEADVGVYFCQGTRTP 120
Db 56 YQKQKSPQLLVYNAXTLADGVPSRFSRSGTQSLKINSIQPEDFGSYCYQHHSGIP 115

Qy 121 PTFGGGTVKEIKRTVAAPSFIIPPPSDEOLKSGTASVCLLNNEYPREAKVQWKVDNALQ 180
Db 116 FTFGGGTVKEIKRADAAPTVSIIPPPSDEOLKSGTASVCLLNNEYPKDINVKWKIDGSR 175

Qy 181 SGNQSQSVTEQDSKDSYSLSSLTLSKADYKHVKYACVETHQGLSSPVTKSFNRGEC 239
Db 181 QNGVLNSWTDQDSKDSYSSMTLTITKDEYERHNSYTCETHTKTSTSPIVKSFNRNEC 234

RESULT 6
Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; ig; 2.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match 55.0%; Score 682.5; DB 11; Length 234;
Best Local Similarity 55.2%; Pred. No. 3e-56;
Matches 132; Conservative 35; Mismatches 67; Indels 5; Gaps 1;

Qy 1 MSLPAQLGLLLLCVPGSSGEVVMVTPGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MMSSAQFLGLLLLCFQGTGTRCDIQMTQTSSLSASLGDRVTISCRASQDISN-----YLNW 55

Qy 61 YQKPGQPRLIIYKVNRSQVDPDRFSGSGAGTDTFTLKISAVEADVGVYFCQGTRTP 120
Db 56 YQKPGDGTVKLLIYTSRLYLGVPFSRFSGSGGTDYSLTISNLEQEDIATYFCQGGTTPP 115

Qy 121 PTFGGGTVKEIKRTVAAPSFIIPPPSDEOLKSGTASVCLLNNEYPREAKVQWKVDNALQ 180
Db 116 FTFGGGTVKEIKRADAAPTVSIIPPPSDEOLKSGTASVCLLNNEYPKDINVKWKIDGSR 175

Qy 181 SGNQSQSVTEQDSKDSYSLSSLTLSKADYKHVKYACVETHQGLSSPVTKSFNRGEC 239
Db 176 QNGVLNSWTDQDSKDSYSSMTLTITKDEYERHNSYTCETHTKTSTSPIVKSFNRNEC 234

RESULT 7
Q8R062 PRELIMINARY; PRT; 234 AA.
AC Q8R062;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418; AAH27418.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 53.9%; Score 669.5; DB 11; Length 234;
Best Local Similarity 54.4%; Pred. No. 5e-55;
Matches 130; Conservative 38; Mismatches 66; Indels 5; Gaps 1;

Qy 1 MSLPAQLGLLLLCVPGSSGEVVMVTPGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MMSSAQFLGLLLLCFQGTGTRCDIQMTQTSSLSASLGDRVTISCRASQDISN-----YLNW 55

Qy 61 YQKPGQPRLIIYKVNRSQVDPDRFSGSGAGTDTFTLKISAVEADVGVYFCQGTRTP 120
Db 56 YQKPGDGTVKLLIYTSRLYLGVPFSRFSGSGGTHYSLTISNLEPEDIATYCYQSYQFP 115

Qy 121 PTFGGGTVKEIKRTVAAPSFIIPPPSDEOLKSGTASVCLLNNEYPREAKVQWKVDNALQ 180
Db 116 FTFGGGTVKEIKRADAAPTVSIIPPPSDEOLKSGTASVCLLNNEYPKDINVKWKIDGSR 175
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Db 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
RESULT 2
Q8VC16 PRELIMINARY; PRT; 238 AA.
AC Q8VC16;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=COLON;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 69.6%; Score 864.5; DB 11; Length 238;
Best Local Similarity 68.2%; Pred. No. 2.2e-73;
Matches 163; Conservative 30; Mismatches 45; Indels 1; Gaps 1;

QY 1 MSIPAQLLGLLLCVPGSSGEVVMVTQSLPLPTGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MKLPVRL--VLMFWIPASSSDVVMVTQTPLSLPVLGDQASISCRSSQSLVHSNGNTYLEW 59

QY 61 YQKPGQPRLIIYKVSNRDVGVPDRFSGSGAGTDFTLKISAVEADVGVPFCGGQTRTP 120
Db 60 YLQKPGSQPKLLIYKVSNRFSGVDPDRFSGSGTDFTLKISRVEADLGVYFCSTHVP 119

QY 121 PTFGGKTVEIKETVAAPSVFIPPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQ 180
Db 120 PTFGGKTLEIKRADAAPTVSIIPPSSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSR 179

QY 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 180 QNGVLNSWTDQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRNEC 238

Query Match 69.6%; Score 864.5; DB 11; Length 238;
Best Local Similarity 68.2%; Pred. No. 2.2e-73;
Matches 163; Conservative 30; Mismatches 45; Indels 1; Gaps 1;

QY 1 MSIPAQLLGLLLCVPGSSGEVVMVTQSLPLPTGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MKLPVRL--VLMFWIPASSSDVVMVTQTPLSLPVLGDQASISCRSSQSLVHSNGNTYLEW 59

QY 61 YQKPGQPRLIIYKVSNRDVGVPDRFSGSGAGTDFTLKISAVEADVGVPFCGGQTRTP 120
Db 60 YLQKPGSQPKLLIYKVSNRFSGVDPDRFSGSGTDFTLKISRVEADLGVYFCSTHVP 119

QY 121 PTFGGKTVEIKETVAAPSVFIPPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQ 180
Db 120 PTFGGKTLEIKRADAAPTVSIIPPSSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSR 179

QY 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 180 QNGVLNSWTDQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRNEC 238

RESULT 3
Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020355; AAH02035.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003599; Ig.
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DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 67.9%; Score 843.5; DB 11; Length 238;
Best Local Similarity 66.5%; Pred. No. 2.1e-71;
Matches 159; Conservative 33; Mismatches 46; Indels 1; Gaps 1;

QY 1 MSIPAQLLGLLLCVPGSSGEVVMVTQSLPLPTGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MKLPVRL--VLMFWIPASSSDVVMVTQTPLSLPVLGDQASISCRSSQSLVHSNGNTYLEW 59

QY 61 YQKPGQPRLIIYKVSNRDVGVPDRFSGSGAGTDFTLKISAVEADVGVPFCGGQTRTP 120
Db 60 YLQKPGSQPKLLIYKVSNRFSGVDPDRFSGSGTDFTLKISRVEADLGVYFCQSHVP 119

QY 121 PTFGGKTVEIKETVAAPSVFIPPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQ 180
Db 120 YTFGSGTKLEIKRADAAPTVSIIPPSSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSR 179

QY 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 180 QNGVLNSWTDQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRNEC 238

RESULT 4
Q8VC55 PRELIMINARY; PRT; 239 AA.
AC Q8VC55;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=COLON;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021781; AAH21781.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;

Query Match 65.1%; Score 808; DB 11; Length 239;
Best Local Similarity 64.4%; Pred. No. 4.7e-68;
Matches 154; Conservative 32; Mismatches 53; Indels 0; Gaps 0;

QY 1 MSIPAQLLGLLLCVPGSSGEVVMVTQSLPLPTGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MKLPVLLVLLLTSPASSSDVVLVTQTPLSLPVLGDQASISCKTSLNSDGFYLDW 60

QY 61 YQKPGQPRLIIYKVSNRDVGVPDRFSGSGAGTDFTLKISAVEADVGVPFCGGQTRTP 120
```

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 21.6765 Seconds
(without alignments)
2271.829 Million cell updates/sec

Title: US-09-758-173-6
Perfect score: 1242
Sequence: 1 MSLPAQLGLLLLCVPGSSG.....EVTHQGLSSPTKSPNRGEC 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1103	88.8	239	4 Q8TCD0	Q8Tcd0 homo sapien
2	864.5	69.6	238	11 Q8VC16	Q8vc16 mus musculus
3	843.5	67.9	238	11 Q9NM37	Q9nm37 mus musculus
4	808	65.1	239	11 Q8VC55	Q8vc55 mus musculus
5	691.5	55.7	234	11 Q8VCP0	Q8vcp0 mus musculus
6	682.5	55.0	234	11 Q91WF8	Q91wf8 mus musculus
7	669.5	53.9	234	11 Q8R062	Q8r062 mus musculus
8	667	53.7	235	11 Q81W12	Q81w12 mus musculus
9	656.5	52.9	234	11 Q8R028	Q8r028 mus musculus
10	655.5	52.8	233	11 Q91W59	Q91w59 mus musculus
11	638.5	51.4	214	11 Q91R1A5	Q91r1a5 mus musculus
12	462.5	37.2	114	4 Q9UL80	Q9ul80 homo sapien
13	460.5	37.1	233	4 Q8TBC9	Q8tbc9 homo sapien
14	437.5	35.2	237	4 Q8WTU6	Q8wtu6 homo sapien
15	434.5	35.0	237	4 Q8WUK4	Q8wuk4 homo sapien
16	427	34.4	104	11 Q9JL82	Q9jl82 mus musculus

17	408	32.9	236	4 Q96B61	Q96b61 homo sapien
18	380	30.6	235	11 Q99W11	Q99w11 mus musculus
19	379.5	30.6	233	4 Q96169	Q96169 homo sapien
20	375	30.2	109	4 Q9UL78	Q9ul78 homo sapien
21	362.5	29.2	240	4 Q8WUK3	Q8wuk3 mus musculus
22	353.5	28.5	111	11 Q920E9	Q920e9 mus musculus
23	350	28.2	109	4 Q9UL85	Q9ul85 homo sapien
24	342.5	27.6	108	4 Q9UL83	Q9ul83 homo sapien
25	342	27.5	109	4 Q9UL86	Q9ul86 homo sapien
26	333.5	26.9	107	11 Q9ERZ9	Q9erz9 mus musculus
27	329.5	26.5	103	11 Q9JL80	Q9jl80 mus musculus
28	329.5	26.5	108	4 Q9UL79	Q9ul79 homo sapien
29	326	26.2	134	11 Q8VDD0	Q8vdd0 mus musculus
30	324	26.1	107	4 Q96SA9	Q96sa9 homo sapien
31	322.5	26.0	108	4 Q9UL77	Q9ul77 mus musculus
32	314.5	25.3	108	4 Q9UL70	Q9ul70 homo sapien
33	312.5	25.2	99	11 Q9JL74	Q9jl74 mus musculus
34	309.5	24.9	298	11 Q9QYF0	Q9qyf0 mus musculus
35	309	24.9	107	4 Q9UL81	Q9ul81 homo sapien
36	306.5	24.7	108	11 Q8VIJ0	Q8vij0 mus musculus
37	306.5	24.7	127	11 Q925S9	Q925s9 mus musculus
38	299.5	24.1	116	4 Q96PF6	Q96pf6 homo sapien
39	297.5	24.0	109	11 Q920E6	Q920e6 mus musculus
40	293	23.6	106	5 Q9U410	Q9u410 schistosoma
41	289.5	23.3	101	11 Q9JL78	Q9jl78 mus musculus
42	286.5	21.5	109	6 Q9N0W5	Q9n0w5 oryctolagus
43	265.5	21.4	97	11 Q9JL76	Q9jl76 mus musculus
44	260.5	21.0	107	11 Q9JL84	Q9jl84 mus musculus
45	238	19.2	241	11 Q921A6	Q921a6 mus musculus

ALIGNMENTS

RESULT 1

Q8TCD0	PRELIMINARY;	PRT;	239 AA.
ID	Q8TCD0	PRELIMINARY;	PRT;
AC	Q8TCD0;		
DT	01-JUN-2002 (TrEMBLrel. 21, Created)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DE	Hypothetical 26.2 kDa protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LUNG;		
RA	Strausberg R.;		
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC023362; AAH22362.1; -		
KW	Hypothetical protein.		
SQ	SEQUENCE 239 AA; 26234 MW; FACEDCA3B03871D CRC64;		

Query Match	88.8%;	Score 1103;	DB 4;	Length 239;
Best Local Similarity	88.7%;	Pred. No. 7.6e-96;		
Matches 212;	Conservative 15;	Mismatches 12;	Indels 0;	Gaps 0;
Oy	1	MSLPAQLGLLLLCVPGSSGEVMTQSLPTTPGPASISCRSSQSLKHSNGDTPLSW	60	
Db	1	MRLPAQLGLLMLVPGSSGDVMTQSLPTTPGPASISCRSTQSLVSDGNTYLNW	60	
Oy	61	YQKPGOPRLLIYKVNRSNDGVPDRFSGSGAGTDFTLTKISAVEAEADVGVFCQGRTPT	120	
Db	61	FQKPGOPRLLIYKVNRSNDGVPDRFSGSGAGTDFTLTKITRVEAEADVGVFCQGHWP	120	
Oy	121	PTFGGKTVEIKRTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ	180	
Db	121	STFGGKTLEIKRTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ	180	
Oy	181	SGNSQESVTQDSKDSYISLSTLTLSKAYEKHYKACVTHQGLSSPTKSPNRGEC	239	

Db 180 HREDYNSTLRVVSALPIQHODWMSGKEFKYNNRSLPPIETKSKPGVPRAQVYL 239
QY 383 PPSRDELTKQVSLTCLVKGFPYSDIAVWESNGQPNKYKTPPVLDSDGSFFLYSKLT 442
Db 240 PPAEEMTKKEFSLTGMITGFLPAEIAVDWTSNGRTEQYKNTATVLDSDGSYFYMSKL 299
QY 443 VDKSRVQOQNVFSCSVMHAEALHNYTKSLSPGK 478
Db 300 VQKSTWERSLFACSVVHEVLHNLTKTISRSLGK 335

RESULT 15

GCAM MOUSE STANDARD; PRT; 399 AA.
AC P01865;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE Ig gamma-2A chain C region, Last annotation update)
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
SEGMENT OF MU CHAINS.
CC -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
THE A ALLELE.
CC
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CC EMBL; J00471; AAB59661.1; ALT_INIT.
DR PIR; A02154; G2MSGAM.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT TRANSMEM 346 363
FT DOMAIN 364 399
FT CARBOHYD 180 180
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;
Query Match 43.6%; Score 1117; DB 1; Length 399;
Best Local Similarity 63.4%; Pred. No. 4e-72;
Matches 210; Conservative 43; Mismatches 74; Indels 4; Gaps 3;
QY 149 ASTKGPSVFLPLAPSSKTSGGTAALGCLVKGFPYSDIAVWESNGALTSVGHVHTPAVLQSS 208
Db 1 AKTTAPSVYFLAPVCGDTTGGSSVTGLCLVKGFPYSDIAVWESNGALTSVGHVHTPAVLQSD 60
QY 209 GLYSLSSVWTVPSSSLGTQTYICNVNHNKPSNTKVDDKABPKSCDKTHTCPP--CPAPELL 266
Db 61 -LYTLSSSVTVTSSTWPSQSIITCNVAHPASSTKVDDKIEPRG-PTIKPCPCPKCPAPNLL 118
QY 267 GGPSVFLPPPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 326
Db 119 GGPSVFIFPPPKIKDVLMLISLSPITCVVDVSDDDPDQVQISWFWNNVVEVHTAQTQTHRED 178
QY 327 YNSTYRVVSVLTVLHODWLNKGVCKVSNKALPAPIETKTSKAKGQPREPOVYVTLPPSR 386
Db 179 YNSTLRVVSALPIQHODWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQYVYLPPPE 238
QY 387 DELTKNQVSLTCLVKGFYPSDIAVWESNGQPNKYKTPPVLDSDGSFFLYSKLTVDKS 446
Db 239 EEMTKQVTLTCVTDMPEDIVVENTNNGKTELNYKNTPEVLDSDGSYFYMSKLAVEKK 298
QY 447 RWQGNVFSVSMHEALHNYTKSLSPG 477
Db 299 NWVERNSYSCSVVHEGLHNNHTTKSFRTPG 329

Search completed: March 29, 2003, 09:11:15
Job time : 12.3969 secs

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RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446 (1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=7417517; PubMed=4931970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications
RT for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435 (1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=7305687; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462 (1972).
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CC -----
CC EMBL; V00798; CAA24178.1; -.
DR PIR; A02152; G2MSA.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region.
KW NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
FT SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;
SQ
Query Match 43.8%; Score 1122; DB 1; Length 330;
Best Local Similarity 63.6%; Pred. No. 1.4e-72;
Matches 211; Conservative 43; Mismatches 74; Indels 4; Gaps 3;
QY 149 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 208
DB 1 AKTAPSVYPLPVCGDITGSSVTLGCLVKGYFPEPTLTWNSGSLSSGVTTPAVLQSD 60
QY 209 GLYSLSVWTVPSSSLGTOTYICNVNHPKSNKTKVKKAEPSKCDKTHTCPP--CDAPELL 266
DB 61 -LYTLSSVTVTSSTWPSQGITCNVHPASTKVDKKIEPRG-PTIKPCPCPCAPNLL 118
QY 267 GGSFVFLFPKPKDMLISRTPEVTCVVDVSHDEPEVKFNVDGVVHNAKTPREQ 326
DB 119 GGSFVIFPPKIKDVLMSLSPIVTCVVDVSDDDPDVQISFNVNVEVHTAQTHRED 178
QY 327 YNSTYRVVSVLTVLHQLDNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 386
DB 179 YNSTLRVVSALPIQHQQDMSGKFEKCKVNNKQLPAPFIERTISKPKSGVSRAPQVYVLPPE 238
QY 387 DELTKQVSLTCLVKGFPYPSDIAVEESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKS 446
DB 239 EMTTKKQVLTICMTDMPEDPIYEVETWNGKTELTNYKTEPEVLDSDGSIFMYSKLRVEKK 298
QY 447 RWQGNVSCSVMHLEALHNNHYTKQSLSPGK 478

Db 299 NMVERNSYSCSVVHGLHNNHTTKSFSTPGK 330
RESULT 14
GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT IgG2aa and IgG2ab alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499 (1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain Fc regions of Ig1a and Ig1b allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035 (1981).
CC -!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
CC -----
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CC -----
CC EMBL; J00479; -. NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region.
KW NON_TER 1
FT SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
SQ
Query Match 43.7%; Score 1119.5; DB 1; Length 335;
Best Local Similarity 61.3%; Pred. No. 2.1e-72;
Matches 206; Conservative 52; Mismatches 71; Indels 7; Gaps 2;
QY 149 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 208
DB 1 AKTAPSVYPLPVCGDITGSSVTLGCLVKGYFPEPTLTWNSGSLSSGVTTPAVLQ-S 59
QY 209 GLYSLSVWTVPSSSLGTOTYICNVNHPKSNKTKVKKAEPK-----SCDKTHTCPPCPA 262
DB 60 GLYTLSSVTVTSSTWPSQGITCNVHPASTKVDKKIEPRVPTQNCPHPQHVPPCAA 119
QY 263 PELGGPSVFLFPKPKDMLISRTPEVTCVVDVSHDEPEVKFNVDGVVHNAKTKP 322
DB 120 PDLLGGPSVFIFFPKIKDVLMSLSPMVTCVVDVSDDDPDVQISWFFNVNVEVHTAQTOT 179
QY 323 REEQNSTYRVVSVLTVLHQLDNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 382
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Db 1 AKTTPSVYPLAPGSAQTNSMTLGLVKGYPPEVTVTWNSGLSSGVHTTPAVLQSD 60
 Qy 209 GLYSLSSVTVPSSESLGTQTYICNVNHPKSTKVDKKAEPKSCDKHTCTCP--CPAPELL 266
 Db 61 -LITLSSVTVPSPPSTVTCNVNAHPASSTKVDKILVPRDCG---CKPCICTVPEV- 114
 Qy 267 GGSFVLFPKPKDMLISRTPEVTCVVDVSHDEPEVKFNWYDGVGVHNAKTKPREEQ 326
 Db 115 --SSVFIFPKPKDVLITLTLPKVCVVDVSKDPEVQFSWFVDDVEVHTAQTPREEQ 172
 Qy 327 YNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKTSKAKGPRPOVYVTPPSR 386
 Db 173 FNTSFVSELPMHODWLNKGEYKCKVSNKALPAPIETKTSKAKGPRPOVYVTPPSR 232
 Qy 387 DELTKNQVSLTCLVKGYPDSIAVWESNGOPENNYKTPPVLSDSGSFFLYSKLTVDKS 446
 Db 233 EQMAKDKVSLTCLMIDFFPDITVWQWNGQPAENYKNTQPMINTNGSYFVYSLVNVQS 292
 Qy 447 RMOQGVFSCSVMEALHNNHYTKSLSPG 477
 Db 293 NWEAGNTFTCSVLHGLHNNHTKSLSPG 323

RESULT 12
 GC3M_MOUSE STANDARD; PRT; 398 AA.
 AC P03987;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma-3 chain C region, membrane-bound form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85027161; PubMed=6092053;
 RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA Tucker P.W., Blattner F.R.;
 RT "Structural analysis of the murine IgG3 constant region gene."
 RL EMBO J. 3:2041-2046(1984).
 RN [2]
 RP SEQUENCE OF 328-398 FROM N.A.
 RX MEDLINE=84041483; PubMed=6314258;
 RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
 RA Wall R.;
 RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
 segment."
 RL Nucleic Acids Res. 11:6775-6785(1983).
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 CC -----
 DR EMBL; J00451; AAB59655.1; -
 DR EMBL; V01526; CAA24767.1; ALT_SEQ.
 DR PIR; A02155; G3MSM.
 DR HSSP; P01857; 1FC1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003600; Ig_Like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; Ig_Like; 1.
 DR SMART; SM00407; IGCL; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Transmembrane; Alternative splicing.
 FT NON_TER * 1 1

FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 223 CH2.
 FT TRANSMEM 224 327 CH3.
 FT DOMAIN 328 362 POTENTIAL.
 FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
 FT CONFLICT 333 333 E -> G (IN REF. 2).
 FT CONFLICT 342 342 E -> Q (IN REF. 2).
 FT CONFLICT 388 388 P -> F (IN REF. 2).
 SQ SEQUENCE 398 AA; 43929 MW; CF7F64850A41B95 CRC64;
 Query Match 44.0%; Score 1126; DB 1; Length 398;
 Best Local Similarity 63.8%; Freq. No. 9.1e-73;
 Matches 210; Conservative 46; Mismatches 69; Indels 4; Gaps 3;
 Qy 150 STKGPSVFLPAPSCKSTGTAALGCLVKVDYFPEPTVSNWNSGALTSGVHTFPAVLQSSG 209
 Db 1 TTPAPSVYFLVPCSDTSSTSSVTLGCLVKGYFPEPTVKNWYSGLVSSGVRTVSSVLO-SG 59
 Qy 210 LYSLSVVTVPSSSLGTYICNVNHPKSTKVDKKAEPKSCDKHTCTCP--PCPAPELLG 267
 Db 60 FYSLSLVTVPSSTWPSQTVICNVAHPASKTELKRIEPR-IPKPSPPGSSCPGNIILG 118
 Qy 268 GPSVFLFPKPKDMLISRTPEVTCVVDVSHDEPEVKFNWYDGVGVHNAKTKPREEQ 327
 Db 119 GPSVFLFPKPKDMLISRTPEVTCVVDVSHDEPEVKFNWYDGVGVHNAKTKPREEQ 178
 Qy 328 NSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKTSKAKGPRPOVYVTPPSR 387
 Db 179 NSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKTSKAKGPRPOVYVTPPSR 238
 Qy 388 ELTKNQVSLTCLVKGYPDSIAVWESNGOPENNYKTPPVLSDSGSFFLYSKLTVDKSR 447
 Db 239 QMAKKVSLTCLVTFNPFSEALSVWERNGELEQDYKNTPTPLSDSGTYFVYSLVTVTDS 298
 Qy 448 WQOGNVFSCSVMEALHNNHYTKSLSP 476
 Db 299 WQOGNVFSCSVMEALHNNHYTKSLSP 327

RESULT 13
 GCAA_MOUSE STANDARD; PRT; 330 AA.
 AC P01863;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ig gamma-2A chain C region, A allele.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81076554; PubMed=6777755;
 RA Sikorav J.-L., Auffray C., Rougeon F.;
 RT "Structure of the constant and 3' untranslated regions of the murine
 RT Balb/c gamma 2a heavy chain messenger RNA."
 RL Nucleic Acids Res. 8:3143-3155(1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81198976; PubMed=6262729;
 RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
 RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
 RT and evolution of heavy chain genes; further evidence for intervening
 RT sequence-mediated domain transfer."
 RL Nucleic Acids Res. 9:1365-1381(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81223894; PubMed=6787604;
 RA Ollio R., Auffray C., Morchamps C., Rougeon F.;
 RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
 RT suggests that exons can be exchanged between genes in a multigenic

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CC -----
 CC EMBL: J00451; -; NOT_ANNOTATED_CDS.
 CC PIR: B02156; GIMSC.

DR HSP; P01857; IFCL.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003600; Ig_like.

DR Pfam; PF00047; Ig_3.

DR SMART; SM00410; Ig_like; 1.

DR SMART; SM00407; IGc1; 2.

DR PROSITE; PS00290; Ig_MHC; 1.

DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

KW Transmembrane; Alternative splicing.

FT NON TER 1 1

FT DOMAIN 1 97 CH1.

FT DOMAIN 98 113 HINGE.

FT DOMAIN 114 223 CH2.

FT DOMAIN 224 327 CH3.

SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 44.4%; Score 1137; DB 1; Length 329;

Best Local Similarity 64.0%; Pred. No. 1.2e-73;

Matches 212; Conservative 46; Mismatches 69; Indels 4; Gaps 3;

Qy 150 STKGPSVFLPAPSKSTSGTAAALGLVDPYFVTVSWNSGALTSGVHTFPVAVLQSSG 209

Db 1 TTTAPSVFLPAPSKSTSGTAAALGLVDPYFVTVSWNSGALTSGVHTFPVAVLQSSG 59

Qy 210 LYLSSVTVTPSSSLGTQYICNVNHPKNTKDKKAPKSCDKTHTCP--PCPAPELLG 267

Db 60 FYSLSLVTVTPSSSLGTQYICNVNHPKNTKDKKAPKSCDKTHTCP--PCPAPELLG 118

Qy 268 GPSVFLPAPSKSTSGTAAALGLVDPYFVTVSWNSGALTSGVHTFPVAVLQSSG 327

Db 119 GPSVFLPAPSKSTSGTAAALGLVDPYFVTVSWNSGALTSGVHTFPVAVLQSSG 178

Qy 328 NSTYRVVSVLTVLQDNLNGKEYCKVSKNKAIPATIKSKAKQRPQVYTLPPSRD 387

Db 179 NSTYRVVSVLTVLQDNLNGKEYCKVSKNKAIPATIKSKAKQRPQVYTLPPSRD 238

Qy 388 ELTKNVSITCLVKGYPSPDIKAVESNCPENNYKTPPVLDSDGSPFLYSKLTVDKSR 447

Db 239 QMSKKVSVLTVLQDNLNGKEYCKVSKNKAIPATIKSKAKQRPQVYTLPPSRD 298

Qy 448 WQGNVFCVSMHEALHNYHTQKSLSPGK 478

Db 299 WLQGEIFTCVSVHEALHNYHTQKSLSPGK 329

RESULT 11

ID GC1M MOUSE STANDARD; PRT; 393 AA.

AC P01859;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Ig gamma-1 chain C region, membrane-bound form.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=80045036; PubMed=115593;

RA Honjo T., Obara M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,

RA Takahashi N., Mano Y.;

RT "Cloning and complete nucleotide sequence of mouse immunoglobulin

gamma 1 chain gene.";

RL Cell 18:559-568(1979).

RN [2]

RP SEQUENCE OF 323-393 FROM N.A.
 RX MEDLINE=82197626; PubMed=6804950;
 RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;

RT "mRNA for surface immunoglobulin gamma chains encodes a highly

conserved transmembrane sequence and a 28-residue intracellular

domain.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).

RN [3]

RP SEQUENCE OF 323-366 FROM N.A.

RX MEDLINE=82115295; PubMed=6799207;

RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,

RA Eisenberg D., Wall R.;

RT "Gene segments encoding transmembrane carboxyl termini of

immunoglobulin gamma chains.";

RL Cell 26:19-27(1981).

RN [4]

RP SEQUENCE OF 1-44 FROM N.A.

RX MEDLINE=8222190; PubMed=6283537;

RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;

RT "Nucleotide sequences of gene segments encoding membrane domains of

immunoglobulin gamma chains.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA

SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED

GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-

BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED

IN SEPARATE EXONS. THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND

SEGMENT OF MU CHAINS.

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CC EMBL; V00793; CAA24172.1; -.

DR EMBL; V00793; CAA24173.1; -.

DR EMBL; V00793; CAA24174.1; -.

DR PIR; B02159; G1MSM.

DR HSSP; P01842; 7FAB.

DR MGD; MGI:96446; Igh-4.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003597; Ig_c1.

DR Pfam; PF00047; Ig_3.

DR SMART; SM00407; IGc1; 2.

DR PROSITE; PS00290; Ig_MHC; 1.

DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

KW Alternative splicing; Transmembrane.

FT NON TER 1 1

FT DOMAIN 1 97 CH1.

FT DOMAIN 98 110 HINGE.

FT DOMAIN 111 217 CH2.

FT DOMAIN 218 324 CH3.

FT DISULFID 27 82

FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 138 198

FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).

FT DISULFID 244 302

FT TRANSMEM 340 357 POTENTIAL.

FT DOMAIN 358 393 CYTOPLASMIC (POTENTIAL).

SQ SEQUENCE 393 AA; 43386 MW; 4CC8B343B7A1CE27 CRC64;

Query Match 44.2%; Score 1133; DB 1; Length 393;

Best Local Similarity 61.9%; Pred. No. 2.9e-73;

Matches 205; Conservative 55; Mismatches 61; Indels 10; Gaps 4;

Qy 149 ASTKGPSVFLPAPSKSTSGTAAALGLVDPYFVTVSWNSGALTSGVHTFPVAVLQSS 208

Db 1 TTTAPSVFLPAPSKSTSGTAAALGLVDPYFVTVSWNSGALTSGVHTFPVAVLQSS 59

Qy 210 LYLSSVTVTPSSSLGTQYICNVNHPKNTKDKKAPKSCDKTHTCP--PCPAPELLG 267

Db 60 FYSLSLVTVTPSSSLGTQYICNVNHPKNTKDKKAPKSCDKTHTCP--PCPAPELLG 118

Qy 268 GPSVFLPAPSKSTSGTAAALGLVDPYFVTVSWNSGALTSGVHTFPVAVLQSSG 327

Db 119 GPSVFLPAPSKSTSGTAAALGLVDPYFVTVSWNSGALTSGVHTFPVAVLQSSG 178

Qy 328 NSTYRVVSVLTVLQDNLNGKEYCKVSKNKAIPATIKSKAKQRPQVYTLPPSRD 387

Db 179 NSTYRVVSVLTVLQDNLNGKEYCKVSKNKAIPATIKSKAKQRPQVYTLPPSRD 238

Qy 388 ELTKNVSITCLVKGYPSPDIKAVESNCPENNYKTPPVLDSDGSPFLYSKLTVDKSR 447

Db 239 QMSKKVSVLTVLQDNLNGKEYCKVSKNKAIPATIKSKAKQRPQVYTLPPSRD 298

Qy 448 WQGNVFCVSMHEALHNYHTQKSLSPGK 478

Db 299 WLQGEIFTCVSVHEALHNYHTQKSLSPGK 329

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RESULT 9
GC1_MOUSE
ID GC1_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
RT cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salser W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
RT heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=78242288; PubMed=98524;
RA Adefuogo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
RT murine myeloma gamma chain.";
RL J. Biol. Chem. 253:6068-6075(1978).
RN [5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulfide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
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CC -----
DR EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR EMBL; V00793; CAA24175.1; -
DR EMBL; V00795; CAA24176.1; -
DR PIR; A02159; GIMS.
DR HSP; P01842; 7FAB.
DR GlycoSuiteDB; P01868; --
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003006; Ig_MHC.
DR InEPR; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

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KW Alternative splicing.
FT NON_TER 1 97
FT DOMAIN 98 110 CH1.
FT DOMAIN 111 217 HINGE.
FT DOMAIN 218 324 CH2.
FT DISULFID 27 82 CH3.
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198 INTERCHAIN (WITH A HEAVY CHAIN).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. .).
FT DISULFID 244 302 /FTID=CAR_000055.
FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
FT CONFLICT 276 276 N -> D (IN REF. 3).
FT CONFLICT 278 278 N -> D (IN REF. 3).
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;

Query Match 44.4%; Score 1138; DB 1; Length 324;
Best Local Similarity 62.0%; Pred. No. 9.9e-74;
Matches 206; Conservative 55; Mismatches 61; Indels 10; Gaps 4;

QY 149 ASTKGPVSFVFLAPSSKSTSGCTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 208
Db 1 AKTPPSVYFLAPGSAQAQNSMTLGLCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 60
QY 209 GLXSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPP--CPAPELL 266
Db 61 -LVTLSSTVPSPSPRPSETVTCNVAHPASSTKVDKKIIVPRDCG----CKPFCITVPEV- 114
QY 267 GGSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQ 326
Db 115 --SSVFIFPPKPKDVLITLTITPKVTCVVVDISKDDPEVPSFVDFVDDVEVHTAQTQPREEQ 172
QY 327 YNSTYRVSVTLVHODWLNKGKEYKCKVSNKALPAPIEKTIKSKAKOPREPVYVTLPPSR 386
Db 173 FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPIEKTIKTKGRKAPQVYVTLPPPK 232
QY 387 DELTKQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVPLDSDGSGFLYSLKLTVDKS 446
Db 233 EQMAKDKVSLTCLMIDTFPPEDITVEWQWNGQPAENYKNTQPIIMNTNGSVFVYSKLVNQS 292
QY 447 RWOQGNVFCSCVMHEALHNYTKQSLSLSPGK 478
Db 293 NWEAGNTFTCSVLHLEGLHHHTKSLSHSPGK 324

RESULT 10
GC3_MOUSE
ID GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
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QY 373 QREPOVYTLPSRDELTKNOVSLCLVKGFYPSDIAVWESNGOPENNYKTTTPPVLDS 432
DB 185 QREPOVYTLPSREBEMTKNOVSLCLVKGFYPSDIAVWESSGGPENNYNTTPMLDSD 244
QY 433 GSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 478
DB 245 GSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 290

RESULT 7
GC1_RAT ID GC1_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 44.8%; Score 1148; DB 1; Length 326;
Best Local Similarity 63.1%; Pred. No. 2e-74;
Matches 210; Conservative 52; Mismatches 61; Indels 10; Gaps 4;

QY 149 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPPPVTVSWNSGALTSGVHTFPAVLQSS 208
DB 1 AETAPSVYPLAPGTALKNSMVTGLCLVKGYFPEPVTVTWNSGALSSGVHTFPAVLQ-S 59
QY 209 GLYSLSSVTVTPSSSLGTOTYICNVNHKPSNTKVDKAEKPKS-----CDKHTCPCPA 268
DB 60 GLYTLTSSVTVPSSTWPSQVTCNVNHPASSTKVDKIVPRNCG--GDCKPC---ICTG 113
QY 269 ---PSVFLFPFKPKDTLMI.SRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 325
DB 114 SEVSSVFIFFPKPKDVLITLTPKVTCCVVDVDSQDDPEVHFSWFVDVEVHTAQTREE 173
QY 326 QYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPS 385
DB 174 QFNSTFRSVSELPILHODWLNKGRTRCKVTSAAFPSPIEKTSKPEGRQVPHVYTNSTP 233
QY 386 RDELTKNOVSLCLVKGFYPSDIAVWESNGOPENNYKTTTPPVLDSGFSFLYSLKLTVDK 445
DB 234 KEEMTQNEVITCVMWKGFPDPIYVEWQNGQPQENYKNTPTPTMDTDSYFLYSLKLVKK 293
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QY 446 SRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 478
DB 294 ERWQGNVTCFVSLHGLHNHHTKSLSHSPGK 326

RESULT 8
GCB_RAT ID GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 44.6%; Score 1142.5; DB 1; Length 333;
Best Local Similarity 63.7%; Pred. No. 4.9e-74;
Matches 214; Conservative 44; Mismatches 69; Indels 9; Gaps 3;

QY 149 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPPPVTVSWNSGALTSGVHTFPAVLQSS 208
DB 1 AQTAPSVYPLAPGCGDTTSSVTGLCLVKGYFPEPVTVTWNSGALSSDVHTFPAVLQ-S 59
QY 209 GLYSLSSVTVTPSSSLGTOTYICNVNHKPSNTKVDKAEKPKS-----CDKHTCPCPA 262
DB 60 GLYTLTSSVTVPSSTWPSQVTCNVNHPASSTKVDKIVPRNCGIGHKCPTCTCHKCPV 117
QY 263 PELIGPSVFLFPFKPKDTLMI.SRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTP 322
DB 118 PELIGPSVFIFFPKPKDILLISQNAKVTICVVVDVSEEPDQVQSFVNNVEVHTAQTQP 177
QY 323 REQYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAKGQPREPQVYTL 382
DB 178 REQYNSTFRVWVSALEPIQHODWLNKGYCKVSNKALPAPIETKISKAKGQPREPQVYV 237
QY 383 PPSRDELTKNOVSLCLVKGFYPSDIAVWESNGOPENNYKTTTPPVLDSGFSFLYSLKLT 442
DB 238 GPPTQETQETQVTLTCLTSGFLPNDIGVETWSNGHLEKNKNTPEVWDSGFSFLYSLKLN 297
QY 443 VDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 478
DB 298 VERSRWDSRAPFVCSVVHGLHNHHTKSLSHSPGK 333
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DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig2.
DR SMART; SM00407; IGc1. 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 V -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 47.9%; Score 1226.5; DB 1; Length 323;
Best Local Similarity 69.7%; Pred. No. 5.2e-80;
Matches 228; Conservative 34; Mismatches 58; Indels 7; Gaps 2;

QY 152 KPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPVTVSWNSGALTSGVHTFPAVLQSSGLY 211
DB 4 KAPSVFPLAPCCGTPSSTVTGLGCLVKGLPPEVTVWNSGTLTGNGVTRTFPSVROSSGLY 63

QY 212 SLSSVTVVPSSSLGTQTYICNVNHPKSNTKVDKAEKPSCKDTHTCPPCAPPELLGGPSV 271
DB 64 SLSSVTVVTSSS---QPVTCNVVAHPATNKVDKTVAPSTCSK----PTCPPPELLGGPSV 116

QY 272 FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 331
DB 117 FLFPPKPKDTLMISRTPEVTCVVDVSDQDDPEVQFTWYINNEQVTRAPPLREQQFNSTI 176

QY 332 RVVSVLTVLHQDWLNGKEYKCKVKNKALPAPIEKTISKAKGQPREPOVYITLPSSDELTK 391
DB 177 RVVSLTPIITHQDWRGKEPKCKVHKNALPAPIEKTISKARGQPLEPKVYTMGPPREEISS 236

QY 392 NOVSLTCLVKGFVPSDIAVEWESNGOPENNYKTTTPVLDSDGSFELYSKLTVDKSRWQQG 451
DB 237 RVVSLTCMNGYFPDSIDISWEKNKGAEDNYKTTTPAVLDSGSLYFLYKNKLSVPTSEWQRG 296

QY 452 NVFSCSVMEALHNHYTQKSLSLSPGK 478
DB 297 DVFTCSVMHEALHNHYTQKSISRSPGK 323

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
OS Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Biraghtein B.K., Hussain Q.Z., Cebra J.J.;

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RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cystine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 47.3%; Score 1212.5; DB 1; Length 329;
Best Local Similarity 70.1%; Pred. No. 5.3e-79;
Matches 234; Conservative 28; Mismatches 63; Indels 9; Gaps 4;

QY 148 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPVTVSWNSGALTSGVHTFPAVLQ 207
DB 1 SARTAPSFVPLAASCVDTSQSMWTLGCLVKGYFPPVTVKNWSGALTSGVHTFPAVLQ- 59

QY 208 SGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKVDKAEKPSCKDTH---TCPPCAPPEL 265
DB 60 SGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKVDKAEKPSCKDTH---TCPPCAPPEL 115

QY 266 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 325
DB 116 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 175

QY 326 QYNSTYRVSVLTPLVHLDWLNKGEYKCKVKNKALPAPIEKTISKAKGQPREPOVYITLPPS 385
DB 326 QYNSTYRVSVLTPLVHLDWLNKGEYKCKVKNKALPAPIEKTISKAKGQPREPOVYITLPPS 385

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16-OCT-2001 (Rel. 40, Last annotation update)
IG gamma-4 chain C region.
IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299862;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192599;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
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CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; G4HU.
DR HSP; P01842; 7FAB.
DR Genew; HGNC:5528; IGHG4.
DR MIM; 147130; --
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003597; Ig C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGH1; 2.
DR PROSITE; PS00290; Ig MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 98
FT CH1.
FT DOMAIN 99 110
FT HINGE.
FT DOMAIN 111 220
FT CH2.
FT DOMAIN 221 327
FT CH3.
FT INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 14 14
FT DISULFID 27 83
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106
FT DISULFID 109 109
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811BF208E7A CRC64;

Query Match 61.9%; Score 1586.5; DB 1; Length 327;
Best Local Similarity 90.6%; Pred No. 1.6e-105;
Matches 299; Conservative 12; Mismatches 16; Indels 3; Gaps 1;

QY 149 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 208
D 1 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
QY 209 GLYSLSSVTVPSSTSGTQTYICNVNPKSNITKVDKAPKSCDKTHCTCPCPAPDELGG 268
D GLYSLSSVTVPSSTSGTQTYICNVNPKSNITKVDKAPKSCDKTHCTCPCPAPDELGG 117
QY 269 PSVFLPPPKPKDTLMISRPETVTVVDSHEDPEVKENYVDGVEVNAKTKPREQYN 328
D PSVFLPPPKPKDTLMISRPETVTVVDSHEDPEVKENYVDGVEVNAKTKPREQYN 177
QY 329 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSQSE 388
D STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSQSE 237

Db 178 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSQSE 237
QY 389 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 448
D LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 297
Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 297
QY 449 QCGNVFSCSVMHHEALHNHYTOKLSLSPGK 478
D QCGNVFSCSVMHHEALHNHYTOKLSLSPGK 327
RESULT 4
GC_RABIT STANDARD; PRT; 323 AA.
ID GC_RABIT
AC F01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-1 haplotype.";
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT immunoglobulin G";
RL Biochem. J. 116:249-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (In) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC -!- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC MARKERS AND REF.5 THE E15 MARKER.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M16426; AAA31289.1; --
DR PIR; A02161; GHRB.
DR HSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.

OX NCBI:TaxID=9606;
 RN [1]
 RP SEQUENCE OF 2-326 FROM N.A.
 RX MEDLINE=82197621; PubMed=6804948;
 RA Ellison J.W., Hood L.E.;
 RT "Linkage and sequence homology of two human immunoglobulin gamma
 heavy chain constant region genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
 RN [2]
 RP SEQUENCE OF 88-115 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=83001943; PubMed=6811139;
 RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
 RT "Structure of human immunoglobulin gamma genes: implications for
 evolution of a gene family.";
 RL Cell 29:671-679(1982).
 RN [3]
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=84235992; PubMed=6329676;
 RA Krawinkel U., Rabbitts T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 genes.";
 RL EMBO J. 1:403-407(1982).
 RN [4]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=8001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 immunoglobulin gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavon monoclonal
 immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
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 CC -----
 DR EMBL: J00230; AAB59393.1; -.
 DR PIR: A02148; G2HU.
 DR HSP: P01857; 1FC1.
 DR Genew; HGNC:5526; IGHG2.
 DR MIM; 147110; -.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00410; Ig_like; 1.
 DR PROSITE; PS00290; IG MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT SITE 156 156
 FT MOD_RES 326 326
 FT VARIANT 60 60
 FT CONFLICT 109 109 C -> S (IN REF. 3).
 FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
 SQ
 Query Match 62.5%; Score 1600; DB 1; Length 326;
 Best Local Similarity 90.9%; Pred. No. 1.7e-106;
 Matches 300; Conservative 12; Mismatches 14; Indels 4; Gaps 2;
 QY 149 ASTKGSVFPLAPSSKSTSGTAAALCLVKDYPEPVTYVSWNSGALTSGVHTFPVQLQS 208
 DB 1 ASTKGSVFPLAPSSKSTSGTAAALCLVKDYPEPVTYVSWNSGALTSGVHTFPVQLQS 60
 QY 209 GLYSLSVVTVPSSSLGTQYICNVNHNKPSNTKVDKAPKSCDKHTTCCPCAPPELLGG 268
 DB 61 GLYSLSVVTVPSSSLGTQYICNVNHNKPSNTKVDKAPKSCDKHTTCCPCAPPELLGG 116
 QY 269 PSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 328
 DB 117 PSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 176
 QY 329 STYRVSVLTIVLQDMWLNKGYCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSRDE 388
 DB 177 STYRVSVLTIVLQDMWLNKGYCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSRDE 236
 QY 389 LTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 448
 DB 237 MTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 296
 QY 449 QQGNVTFSCSVWHEALHNHYTQKSLSLSPGK 478
 DB 297 QQGNVTFSCSVWHEALHNHYTQKSLSLSPGK 326
 RESULT 3
 ID GC4_HUMAN STANDARD; PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nle), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -!- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
CC MARKER & THE GIM (NON-1) MARKERS.
CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35,116,198,269 & 272.
CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198,267&272.
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DR EMBL; J00228; AAC82527.1; ALT_INIT.
DR PIR; A02146; GHU.
DR PDB; 1FC1; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR Genew; HGNC:5525; IGHG1.
DR MIM; 147100; -.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig like; 1.
DR SMART; SM00407; IGH1; 2.
DR PROSITE; PS00290; Ig MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 223 CH2.
FT DOMAIN 224 330 CH3.
FT DISULFID 27 83
FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT MOD_RES 330 330
FT VARIANT 97 97
FT VARIANT 239 239 N-LINKED (GLCNAC...).
FT VARIANT 241 241 REMOVED POST-TRANSLATIONALLY.
FT VARIANT 241 241 K -> R (IN GIM(3) MARKER).
FT VARIANT 241 241 /FTIG=VAR_003886.
FT VARIANT 241 241 D -> E (IN GIM(NON-1) MARKER).
FT VARIANT 241 241 /FTIG=VAR_003887.
FT VARIANT 241 241 L -> M (IN GIM(NON-1) MARKER).
FT VARIANT 241 241 /FTIG=VAR_003888.
FT STRAND 123 126

FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164
FT STRAND 165 166
FT STRAND 175 178
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 206
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 240
FT TURN 241 242
FT STRAND 245 256
FT STRAND 260 266
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;
Query Match 68.8%; Score 1763; DB 1; Length 330;
Best Local Similarity 99.7%; Pred. No. 4.8e-118;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 149 ASTKGSVPFLAPSSKSTGGTAAALCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 208
DB 1 ASTKGSVPFLAPSSKSTGGTAAALCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 209 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKABPKSCDKTHTCPPCPAPPELLGG 268
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKABPKSCDKTHTCPPCPAPPELLGG 120
QY 269 PSVFLPPPKPKDLMISRTPDEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 328
DB 121 PSVFLPPPKPKDLMISRTPDEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 329 STYRVSVLTFLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 388
DB 181 STYRVSVLTFLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 389 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 448
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 449 QQGNVPSCSVMEALHNHYTQKSLSLSPGK 478
DB 301 QQGNVPSCSVMEALHNHYTQKSLSLSPGK 330
RESULT 2
GC2_HUMAN
ID_ GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 11.3969 Seconds
(without alignments)
1739.566 Million cell updates/sec

Title: US-09-758-173-8

Perfect score: 2561

Sequence: 1 MWSLILFLVAVATRVQCE.....MHEALHNHYTKSLSPGK 478

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1763	68.8	330	1 GCI_HUMAN	P01857 homo sapien
2	1600	62.5	326	1 G2_HUMAN	P01859 homo sapien
3	1586.5	61.9	327	1 G4_HUMAN	P01861 homo sapien
4	1226.5	47.9	323	1 GC_RABIT	P01870 oryctolagus
5	1212.5	47.3	329	1 G2_CAVPO	P01862 cavia porce
6	1157	45.2	290	1 G3_HUMAN	P01860 homo sapien
7	1148	44.8	326	1 GCI_RAT	P01867 rattus norv
8	1142.5	44.6	333	1 GCB_RAT	P20759 rattus norv
9	1138	44.4	324	1 GCI_MOUSE	P01868 mus musculu
10	1137	44.4	329	1 G3_MOUSE	P22436 mus musculu
11	1133	44.2	393	1 GCI_MOUSE	P01869 mus musculu
12	1126	44.0	398	1 G3M_MOUSE	P03987 mus musculu
13	1122	43.8	330	1 GCAA_MOUSE	P01863 mus musculu
14	1119.5	43.7	335	1 GCB_MOUSE	P01864 mus musculu
15	1117	43.6	399	1 GCAM_MOUSE	P01865 mus musculu
16	1114.5	43.5	329	1 GCC_RAT	P20762 rattus norv
17	1108	43.3	322	1 GCA_RAT	P20760 rattus norv
18	1085	42.4	336	1 GCB_MOUSE	P01866 mus musculu
19	1080	42.2	405	1 GCBM_MOUSE	P01867 mus musculu
20	489	19.1	428	1 EPC_HUMAN	P01854 homo sapien
21	483.5	18.9	429	1 EPC_RAT	P01855 rattus norv
22	465	18.2	421	1 EPC_MOUSE	P06336 mus musculu
23	448	17.5	455	1 MUC_MOUSE	P01872 mus musculu
24	442	17.3	142	1 HV01_RAT	P01805 rattus norv
25	442	17.3	454	1 MUC_HUMAN	P01871 homo sapien
26	438	17.1	476	1 MUCM_MOUSE	P01873 mus musculu
27	437	17.1	458	1 MUC_RABIT	P03988 oryctolagus
28	430	16.8	144	1 HV26_MOUSE	P01795 mus musculu
29	427	16.7	479	1 MUCM_RABIT	P04221 oryctolagus
30	425	16.6	457	1 MUC_SUNMU	P20768 suncus muri
31	420	16.4	450	1 MUC_CANFA	P01874 canis fami
32	419	16.4	123	1 HV18_MOUSE	P01787 mus musculu
33	418.5	16.3	122	1 HV20_MOUSE	P01789 mus musculu

RESULT 1

ID	GCI_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	IGHG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=82274238; PubMed=6287432;			
RX	Edelson J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Maxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

P01788 mus musculu
P01790 mus musculu
P01786 mus musculu
P06337 mesocricetu
P01791 mus musculu
P01792 mus musculu
P04220 homo sapien
P01794 mus musculu
P01764 homo sapien
P01793 mus musculu
P01801 mus musculu
P23087 heterodontu

ALIGNMENTS

Db 229 STTVDDKLEPSGPTSTINPCPPCKECHKCPAPNLEGPSVFIFPPNKKDVLMLISLTPKVT 288
 QY 292 CVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHODWLNKGEYK 351
 Db 289 CVVVDVSEDDPVOISMFVNNVELTAQOTHRDYNSTIRVVSALPIQODWMSGEFK 348
 QY 352 CKVSNKALPAPLEKTSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSUIAE 411
 Db 349 CKVNNKDLAPAPLEKTSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSUIAE 408
 QY 412 WSNQGNPNYKTPPVLDDSGDFLYSLKTVDKSRWQGNVFCVSNVHEALHNHYTKS 471
 Db 409 WTSNGHTEENTKDTAPVLDDSGDFLYSLKTNMKTSKWKTDSFSCNVRHGLKNYLYLKT 468
 QY 472 LSLSPGK 478
 Db 469 ISRSPGK 475

RESULT 14

I47159
 Ig gamma 2a chain constant region - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: I47159
 R:Kaczkovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A:Title: Five putative subclasses of swine IGH identified from the cDNA sequences of a
 A:Reference number: I47158; MUID:95015845; PMID:7930579
 A:Accession: I47159
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-328 <KAC>
 A:Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124
 C:Genetics:
 A:Gene: IgG2a
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 49.2%; Score 1259; DB 2; Length 328;
 Best Local Similarity 69.3%; Pred. No. 1.8e-67;
 Matches 230; Conservative 43; Mismatches 53; Indels 6; Gaps 2;
 QY 149 ASTKGPSVPLAPSKSTSGTAALGLVKDYFPEPVTVSNVNSGALTSGVHTPAVLQSS 208
 Db 1 APTAPSVYPLAPCSRUTSGFNVALGLASSYFPEPVTVNSGALSSGVHTPFPVLQPS 60
 QY 209 GLYSLSSVTVPSLSLGTQTYICNVNHPKSNKTKVDKGAEPKSCDKHTCTPPCPAPELLGG 268
 Db 61 GLYSLSSMTVPASSLSKSKSYTCNVNHPATTTKVDKRVGTGKTKPPCPICPACESP----G 116
 QY 269 PSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 328
 Db 117 PSVFIFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHTAQTAPKPEQFN 176
 QY 329 STYRVSVVLTVLHODWLNKGEYKCKVSNKALPAPLEKTSKAKGQPREPOVYTLPPSRDE 388
 Db 177 STYRVSVVLPIQODWLNKGEYKCKVNNKDLAPATRIISKAKGQTRPEQVYTLPPHAE 236
 QY 389 LTKNOVSLTCLVKGFPYSDIATAVESNGQ--PNNYKTTTPPVLDDSGDFLYSLKTVDKS 446
 Db 237 LSRKSVITCLVIGYFYPDPDIDVWRNGQPEPEGNRYRTTPPQQDVGDTGYFLYSKFSVDKA 296
 QY 447 RWOQGNVFCVSNVHEALHNHYTKSLSLSPGK 478
 Db 297 SWQGGIFQCAVMHEALHNHYTKSISKTPGK 328

RESULT 15

S31866
 Ig gamma-1 chain C region - synthetic
 C:Species: synthetic

A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
 C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
 C:Accession: S31866
 R:Filipula, D.
 submitted to the EMBL Data Library, February 1993
 A:Description: Screening method for protein-protein interactions of cloned gene products.
 A:Reference number: S31866
 A:Accession: S31866
 A:Molecule type: mRNA
 A:Residues: 1-255 <FIL>
 A:Cross-references: EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PID:G33069
 C:Keywords: immunoglobulin
 F:1-22/Region: Escherichia coli outer membrane protein A precursor
 F:23-255/Region: human Ig gamma-1 chain C region

Query Match 49.0%; Score 1256; DB 4; Length 255;
 Best Local Similarity 97.1%; Pred. No. 2.1e-67;
 Matches 232; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 240 TKVDKKAEPKSCDKHTCTPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSH 299
 Db 17 TVAQADVESKCDKHTCTPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSH 76
 QY 300 EDEPVKFNWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKAL 359
 Db 77 EDEPVKFNWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKAL 136
 QY 360 PAPIEKTISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIATAVESNGQPE 419
 Db 137 PAPIEKTISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIATAVESNGQPE 196
 QY 420 NNYKTTTPPVLDDSGDFLYSLKTVDKSRWQGNVFCVSNVHEALHNHYTKSLSLSPGK 478
 Db 197 NNYKTTTPPVLDDSGDFLYSLKTVDKSRWQGNVFCVSNVHEALHNHYTKSLSLSPGK 255

Search completed: March 29, 2003, 09:16:19
 Job time : 22.453 secs

A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-474 <FIS>
 A:Cross-references: EMBL:X67210; NID:G54826; PIDN:CAA47649.1; PID:G54827
 R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
 Nature 283, 786-789, 1980
 A>Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from H
 A:Reference number: A02157; MUID:80120716; PMID:6766534
 A:Contents: a allele
 A:Accession: A02157
 A:Molecule type: DNA
 A:Residues: 138-161, '1', 163-189, 'FP', 193-474 <YAM>
 A:Cross-references: GB:J00461
 A>Note: The sequence was determined from the germline gene
 R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
 Science 206, 1299-1303, 1979
 A>Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heavy
 A:Reference number: A26235; MUID:80081501; PMID:117548
 A:Contents: MPC 11
 A:Accession: A26235
 A:Molecule type: mRNA
 A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>
 A>Note: Lys-474 is probably removed posttranslationally
 R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
 Science 206, 1303-1306, 1979
 A>Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob
 A:Reference number: A26232; MUID:80081502; PMID:117549
 A:Accession: A26232
 A:Molecule type: DNA
 A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>
 R:Ollo, R.; Rougeon, F.
 Nature 296, 761-763, 1982
 A>Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma
 A:Reference number: A26233; MUID:82173203; PMID:8803173
 A:Contents: b allele
 A:Accession: A26233
 A:Molecule type: DNA
 A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLI>
 A:Cross-references: GB:J00461
 R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi
 J. Biol. Chem. 269, 12345-12350, 1994
 A>Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
 A:Reference number: A53598; MUID:94216359; PMID:7512967
 A:Accession: A53598
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 234-251 <KIM>
 A:Comment: The a allele sequence is shown.
 C:Genetics: 138/1; 236/1; 258/1; 368/1
 A:Introns: 138/1; 236/1; 258/1; 368/1
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotrimer; immunoglobul
 F:157-222/Domain: immunoglobulin homology <IM1>
 F:236-257/Region: hinge
 F:281-350/Domain: immunoglobulin homology <IM2>
 F:387-454/Domain: immunoglobulin homology <IM3>
 F:152/Disulfide bonds: interchain (to light chain) #status predicted
 F:164-220, 288-348, 394-452/Disulfide bonds: #status predicted
 F:247, 250, 253, 256/Disulfide bonds: interchain (to heavy chain) #status predicted
 F:324/Binding site: carbohydrate (asn) (covalent) #status predicted
 Query Match 54.4%; Score 1392; DB 1; Length 474;
 Best Local Similarity 54.6%; Pred. No. 3.8e-75;
 Matches 265; Conservative 73; Mismatches 129; Indels 18; Gaps 4;
 QY 1 MGWSLILFLVAVATPRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
 DB 1 MEWSWIFLLSGTAGVHSEVQLQSGPELVWFGASVMSCKASGYTFYTHYMHVWQKP 60
 QY 61 GKGPEWVGIRNKGNGTTEYAAVSKDRFTISRDDSKSIAYLQMSLKIETDVAVYCTTS 120

DB 61 QGLEWIGYI--NPNKDGTFKFKGKATLTSDKSSNTAYMELSLTSDSAVYVCARD 118
 QY 121 YISHCRGGVCYGVYFPPFWGQCALVTYSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDY 180
 DB 119 YDY-----DWFAWYGQGLTVTVSAAKTTPPSVYPLAPGCGDTTSSVTSCLVKGY 169
 QY 181 FPEPVTVSNWNGALTSQVHTFPVAVLOSGLYSLSVTVPSLSLGTQTYICNVNHPKSN 240
 DB 170 FPEPVTVSNWNGSLSSVHTLSQALQSLYTMSSSVTVPSSTQVTVCSVAHPASST 229
 QY 241 KVDKAPKSCDKT-HTCPP-----CPAPELLGGPSVFLPPPKDKTLMISRTPEVTCV 293
 DB 230 TVDKLEPSPGPISTINPCPKCKECHKCPAPNLEGGPSVFIPEPNKDVLMISLTPEKVTVC 289
 QY 294 VVDVSHEDPEVKFNWVVDGVEVHNNAKTPREQVNSTYRVVSVLTVLHQDWLNGKEYKCK 353
 DB 290 VVDVSEDDPDVQISWFMVNVVHTAQTQTHREDYNSTIRVSTLPIQHQMWSGKEFKCK 349
 QY 354 VSNKALPAPIEKTISKAKGPPEQVYTLPPSRDELTKNOVSLTCLVKGFVPSDIAVEWE 413
 DB 350 VNNKDLSPPIERTISKGLVRAPQVYILPPAEQLSKDYSLTCLVVGPNPGDISVET 409
 QY 414 SNGQPNNYKTPPVLDSDGSPFLSKLTVDKSRWQGNVPSVCSVMHEALHNHYTKSLS 473
 DB 410 SNGTEENYKDTAPVLDSDGSPFIYSKLNMKTSKWEKTSQSPNCVRHGLKNVYLKKTIS 469
 QY 474 LSPGK 478
 DB 470 RSPGK 474
 RESULT 13
 S01321
 Ig gamma-2b chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
 C:Accession: S01321
 R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
 Eur. J. Biochem. 176, 287-295, 1988
 A>Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed ag
 A:Reference number: S01320; MUID:88329081; PMID:3138116
 A:Accession: S01321
 A:Molecule type: mRNA
 A:Residues: 1-475 <DE1>
 A:Cross-references: EMBL:X13188; NID:G51780; PIDN:CAA31580.1; PID:G51781
 A>Note: this sequence was determined from the differentiated gene
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
 F:159-223/Domain: immunoglobulin homology <IMM>
 Query Match 52.3%; Score 1338.5; DB 2; Length 475;
 Best Local Similarity 53.8%; Pred. No. 5.5e-72;
 Matches 262; Conservative 73; Mismatches 131; Indels 21; Gaps 6;
 QY 1 MGWSLILFLVAVATPRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
 DB 1 MEWSWIFLLSGTAGVQSOVQLQSGAELARPAGSVKLSCKASGYTLTSGYSWVKQRT 60
 QY 61 GKGPEWVGIRNKGNGTTEYAAVSKDRFTISRDDSKSIAYLQMSLKIETDVAVYCTTS 120
 DB 61 QGLEWIGYI--YFGSGNSIFNEKFKGKATLTVDKSSSTAYLHLSLTSSEDSAVYFC--- 115
 QY 121 YISHCRGGVCYGVY--FEPWGGALVTYSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVK 178
 DB 116 -----AGPRQVQLLPFGYWGQGLTVTAAKTPPSVYPLAPGCGDTTSSVTLGCLVK 169
 QY 179 DYFPEPVTVSNWNGALTSQVHTFPVAVLOSGLYSLSVTVPSLSLGTQTYICNVNHPKPS 238
 DB 170 GYPESVTVTNWNGSLSSSVHTFFPALQ--SGLYTMSSSVTVPSSTQVTVCSVAHPAS 228
 QY 239 NTKVDKKAEPKCDKT-HTCPP-----CPAPELLGGPSVFLPPPKDKTLMISRTPEVT 291

QY 476 PGK 478
|||
Db 470 PGK 472

RESULT 10

S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
A:Accession: S69339; S72664
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687; PMID:7744049
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamilichi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 55.3%; Score 1415; DB 2; Length 374;
Best Local Similarity 60.2%; Pred. No. 1.3e-76;
Matches 286; Conservative 25; Mismatches 52; Indels 112; Gaps 6;
QY 8 LFLVAVATVQCEVQLVGGGLVPGGSLRVSCAVSGFTFSDH--YMWFRQAPGKGP 65
Db 8 LLLLTTPSWLVSQITLTKESGFLVLPKPTQTTLTCTFSGFSLSKSGVGVGWRQPPGQALE 67
QY 66 WVGFINRKNPGGTEYAASVKDRFTISRDSKSIAYLOWSSLIKIEDTAVYCTTSYISHC 125
Db 68 WLALIFWDDD---KRYSPSLRFLTITKDTSKNQVLTWNVDPADTATYCGYISVEG-- 122
QY 126 RGVCYVG-GY-PEFGQAGALVTVSASTKGPSVFLPAPSSKTSGGTAALGCLVKDYPPE 183
Db 123 -----YCGQYRFHSGQGLVTVSS----- 142
QY 184 PVTVSNNSGALTSGVHTFFAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVD 243
Db 143 ----- 142
QY 244 KKAEPKCDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE 303
Db 143 ---EPKSCDKTHTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE 199
QY 304 VKFNWTVDGVEVHNATKPREQYNSYTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 363
Db 200 VKFNWTVDGVEVHNATKPREQYNSYTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 259
QY 364 EKTISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 423
Db 260 EKTISKAKGQPREPVYTLPPSRDEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 319
QY 424 TTPPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSVNHEALHNHYTQKSLSLSPGK 478
Db 320 TTPPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSVNHEALHNHYTQKSLSLSPGK 374

RESULT 11

S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
A:Accession: S40295

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Froesch, M.; Weisgerber, C.; Bit
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglyutamic acid
F;1-446/Product: Ig gamma-2a chain #status experimental <MAI>
F;1-117/Domain: V-D-J region <VDU>
F;118-446/Domain: C region <CHR>
F;118-214/Domain: C1 region <CH1>
F;215-230/Region: hinge
F;231-340/Domain: C2 region <CH2>
F;341-446/Domain: C3 region <CH3>
F;360-427/Domain: immunoglobulin homology <IMV>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;132/Disulfide bonds: interchain (to light chain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;297/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match 55.3%; Score 1415; DB 2; Length 446;
Best Local Similarity 58.0%; Pred. No. 1.6e-76;
Matches 268; Conservative 69; Mismatches 105; Indels 20; Gaps 6;

QY 20 EVQLVDSGGGLVPGGSLRVSCAVSGFTFSDHYWFRQAPGKGPWVGFIIRKNGGTT 79
Db 1 QIQLOQSGPGLVPGASVKISKASGYTFTDYIHWVKQRPGELEWIGWI--YPGSGNT 58
QY 80 EYAASVKDRFTISRDSKSIAYLOWSSLIKIEDTAVYCTTSYISHCRGGVCGVGYF--EF 137
Db 59 KYNEKFKGKATLTVDTSSSTAYNMQLSLTSSEDSAVYFCAR-----GGKFAMDY 106
QY 138 WGQGALVTSSASTKGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 197
Db 107 WGQGTSVTVSSAKTTPAVVPLAPVCGDITGSSVTLGCLVKGYFPEPTLTWNSSLSG 166
QY 198 VHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKCDKTHTC 257
Db 167 VHTFPAVLQSD-LYTLSSSVTVTSTWPSQITCNVAHPASSTKVDKKEIPRG-PTIKPC 224
QY 258 PP--CPAPELLGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 315
Db 225 PPKCPAPNLLGGPSVFIFFPKIKDVLMSLSLSPWVTCVVDVSEDDPDVQISWFWNVVEV 284
QY 316 HNAKTPREEQYNSYTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQPR 375
Db 285 LTAQTQTHREDYNSLTRVVSALPIQHDWMSGKEFKCKVNNKDLPAPIERTISKPGSVR 344
QY 376 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSP 435
Db 345 APQVYVLPPEPEEMTKKQVTLTCWVDFMPEDIYVEWTNNGKTELNYKNTPEVLDSDGSY 404
QY 436 FLYSKLTVDKSRWQQGNVFCSVNHEALHNHYTQKSLSLSPG 477
Db 405 FMYSKURVEKKKNWERNNSYSCSVVHEGLHNHHTTKFSRTPG 446

RESULT 12

G2MS11
Ig gamma-2b chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
A:Accession: S25057; A26235; A26232; A26233; A53598
R:Fischer, R.; Voss, A.; Nierbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific mc
A:Reference number: S25057
A:Accession: S25057

```
Query Match 57.7%; Score 1478; DB 2; Length 470;
Best Local Similarity 60.9%; Pred. No. 3.1e-80;
Matches 291; Conservative 58; Mismatches 115; Indels 14; Gaps 7;

QY 3 WSLILLFLAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGK 62
DB 5 WT--LLFVLSPAGIVLSQVQLRESGSLVLPKPTSLTCTVSGFSLSYALTWRQAPGK 62
QY 63 GPEWVGFIKPKNGGTEYAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYCYCT- 122
DB 63 ALEWVGSI---TSGGTYYNPALKKRLSITKENSQVSLSSVSTPDTATYYCAR- 117
QY 123 SHCRGGVCYGGYFEPWGGQALVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVDFP 182
DB 118 --TYEVDGGAIDAWGQGLLTVSSASTAPKVPYFLSSCCGDKSSSTVTLGCLVSSYP 175
QY 183 EPTVSWNSGALTSVGHVTPPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKNTKV 242
DB 176 EPTVWNSGALKSGVHTFPAVLQSSGLYSLSMWTVPGSTG-QTFTCNVAHPASSTKV 234
QY 243 DKKAPKSCDKTHTCPPCPAPELLGPGSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDP 302
DB 235 DKAVDP-TC-KSPDCDCPPPELPGSPSVFIPPKPDTLISGTPVTCVVVDVGHDDP 292
QY 303 EVKFNWYDGVVEHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKKYSNKA 362
DB 293 EVKFNWYDGVVEHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKKYSNKA 362
QY 363 IEKTSKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGOP--EN 420
DB 353 IVRTISRTKGPAREQVYVLAPOQELSKSTVSLTCMTWTSFYPDYIAVWQNGOPESD 412
QY 421 NYKTTTPPVLDSDGSPFLSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 478
DB 413 KYGTTPPQLDASSYFLYSKLAVDRNSQEGDTYTCVWHEALHNHYTKQSLSPGK 478

RESULT 8
S37483
IG Gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Ducancel, F.F.D.
A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 57.3%; Score 1467.5; DB 2; Length 469;
Best Local Similarity 57.7%; Pred. No. 1.3e-79;
Matches 277; Conservative 72; Mismatches 118; Indels 13; Gaps 5;

QY 1 MGWSLILLFLAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
DB 1 MGWSLIFLLSGTAGVHCQIQLQSGPELVKPGASVKISCKASGTYTDTYYINWVKQP 60
QY 61 GKEWVGFIKPKNGGTEYAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYCYCT- 120
DB 61 GGLKRWGI--YPASGNTKYNENFGKATLTVDTSSSTAYMLSSLTSEDATVYFC--- 115
QY 121 YISHCRGGVCYGGYFEPWGGQALVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVDF 180
DB 116 ---ARAMGATATLLDYGQGTTLTVSSAKTTPASVYPLAPVCGDITGSSVTLGCLVKG 171
QY 181 FPEPTVSWNSGALTSVGHVTPPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKNT 240
DB 181 FPEPTVSWNSGALTSVGHVTPPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKNT 240

Query Match 55.8%; Score 1429; DB 2; Length 472;
Best Local Similarity 58.4%; Pred. No. 2.5e-77;
Matches 282; Conservative 63; Mismatches 118; Indels 20; Gaps 9;

QY 3 WSLILLFLAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGK 62
DB 3 WT--LLFVLSPAGIVLSQVQLRESGSLATLQTLSTVCTISGFLSNLYGVDWVRQAPG 60
QY 63 GPEWVGFIKPKNGGTE--YAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYCYCT- 118
DB 61 ALEWLG-----GSGDEIDIDYNPVLKSLISITKTSKQVSLTSLTSTVTEDTAVYCAR 114
QY 119 TSY-ISHCRGGVCYGGYFEPWGGQALVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLV 177
DB 115 VDYDSSH--APAYASY-DFWGPGLLISVLSASTTPPKVPLTSCCGDTSSSIVTLGCLV 170
QY 178 KYFPEPTVSWNSGALTSVGHVTPPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPK 237
DB 171 SSMPEPTVTVWNSGALTSVGHVTPPAVLQSSGLYSLSVTVTPASTSGAQTFCNVAHPA 230
QY 238 SNTKVKAKAPKSCDKTHTCPPCPAPELLGPGSVFLPPPKPDTLMISRTPEVTCVVVDV 297
DB 231 SSTKVKRVEPCDPCCKG-CRPPPELPGSPSVFIPPKPDTLISGTPVTCVVVDV 289
QY 298 SHEDPEYKFNWYDGVVEHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKKYSN 357
DB 290 QODDPEYKFNWYDGVVEHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKKYSN 349
QY 358 ALPAPTEKTSKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQ 417
DB 350 ALPAPVTRTISRTKGPAREQVYVLAPOQELSKSTVSLTCLVTFYGYPIAVWQNGQ 409
QY 418 P--BNVKTTPPVLDSDGSPFLSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSP 475
DB 410 PESEDKYGTTSQLDADGSYFLYSRLRVDRNSWQEGDTPACVWHEALHNHYTKQSLSP 469
```

A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A>Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclones. Partial amino acid sequence of the constant
A:Reference number: A90249; MUID:70207560; PMID:4192699
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30; 81-326 <PIN>
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.9%; Score 1586.5; DB 1; Length 327;
Best Local Similarity 90.6%; Pred No. 8.1e-87;
Matches 299; Conservative 12; Mismatches 16; Indels 3; Gaps 1;

Qy 149 ASTKGPVFLPLAASSTSGTAAAGCLVLDYFPEPTVTVNSGALTSQVHTPPAVLQSS 208
Db 1 ASTKGPVFLPLAASSTSGTAAAGCLVLDYFPEPTVTVNSGALTSQVHTPPAVLQSS 60
Qy 209 GLYSLSWVTVVPSSSLTGTQYICNVNHPKSNTPKDKAEPKSCDKTHTCCPAPELLGG 268
Db 61 GLYSLSWVTVVPSSSLTGTQYICNVNHPKSNTPKDKAEPKSCDKTHTCCPAPELLGG 117
Qy 269 PSVFLPPPKPDLMISRTPEVTCVVVDVSHEDPEVKENYVVDGVVHNKTPREOYN 328
Db 118 PSVFLPPPKPDLMISRTPEVTCVVVDVSHEDPEVKENYVVDGVVHNKTPREOYN 177
Qy 329 STYRVSVLVTLHODWLNKGYKCKVSNKALPAPIETKISAKQPREPQVYTLPPSRDE 388
Db 178 STYRVSVLVTLHODWLNKGYKCKVSNKALPAPIETKISAKQPREPQVYTLPPSQEE 237
Qy 389 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 448
Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 297
Qy 449 QOQNVFSCSVWHEALHNHYTQKSLSLSPGK 478
Db 298 QOQNVFSCSVWHEALHNHYTQKSLSLSPGK 327

RESULT 6
FC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: PC4436
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr
A:Reference number: JCS810; MUID:98063277; PMID:9398605
A:Accession: PC4436
A:Molecule type: protein
A:Residues: 1-444 <AKA>
C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed again
C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:251-320/Domain: immunoglobulin homology <IMM>
F:22/Disulfide bonds: interchain (to 98) #status predicted
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 58.4%; Score 1494.5; DB 2; Length 444;
Best Local Similarity 60.5%; Pred No. 3.1e-81;
Matches 279; Conservative 68; Mismatches 95; Indels 19; Gaps 6;

Qy 20 EVQLVESGGGLVQPGGSLRVSCVSGFTFSFHYMYWFRQAPGKGPWGFIRKPNKGGTT 79
Db 1 EVQVETGGGLVRPGNSLCLTSGFTFSYRMHWLRQPPGRKLEWIAVITVKSDNYGA 60
Qy 80 EYAAASVKDRFTISRDDSKSIAYLQMSLLKIEDTAVYCTTYSYSHCRGGVCYGYGFYFWG 139
Db 61 KYAASVGRGFTISRDDSKSVVYLVNRLREEDTATYYC-----CRTPWVYA--MDCWG 111
Qy 140 QGALVTVSSASTKGSVPRLAPSSKSTSGGTAAAGCLVLDYFPEPTVTVNSGALTSQVH 199
Db 112 QGTSVIVSSAKTTPSVVPLAEGSAATQNSMTVGLCLVKGYPPEPTVTVNSGSLSGVH 171
Qy 200 TPAVLOSGLVSLSSVTVVPSSSLTGTQYICNVNHPKSNTPKDKAEPKSCDKTHTCCPP 259
Db 172 TPAVLOSGLVSLSSVTVVPSSSLTGTQYICNVNHPKSNTPKDKAEPKSCDKTHTCCPP 226
Qy 260 --CPAPELLGSPSFLFPPPKPDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHN 317
Db 227 CICTVPEV--SSVFIFFPKPKDVLITLTTPKVTGVVDISKDDPEVQSFVDFVDDVEVHT 283
Qy 318 AKTKPREEOYNSTYRVSVLVTLHODWLNKGYKCKVSNKALPAPIETKISAKQPREP 377
Db 284 AQTPREEOYNSTYRVSVLVTLHODWLNKGYKCKVSNKALPAPIETKISAKQPREP 343
Qy 378 QVTLPPSDELTQKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
Db 344 QVTLPPSDELTQKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 403
Qy 438 YSKLTVDKSRWQOQNVFSCSVWHEALHNHYTQKSLSLSPGK 478
Db 404 YSKLTVDKSRWQOQNVFSCSVWHEALHNHYTQKSLSLSPGK 444

RESULT 7
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S22080; S06610; A31303
R:Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22080
A:Accession: S22080
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-470 <SAN>
A:Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma
A:Reference number: S06610; MUID:90097956; PMID:2513487
A:Accession: S06610
A:Molecule type: DNA
A:Residues: 142-470 <SYM>
A:Cross-references: EMBL:X16701
A>Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: IG CH gamma-1
A:Introns: 98/1; 111/1; 221/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IMM>
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.4%; Score 1624.5; DB 2; Length 377;
 Best Local Similarity 81.7%; Pred. No. 5.4e-89; Indels 47; Gaps 1;
 Matches 300; Conservative 10; Mismatches 12

QY 149 ASTKGPSVFLAPSSKSTSGTAAALCLVQYFPEPTVSWNSGALTSVHTPPAVLQSS 208
 DB 1 ASTKGPSVFLAPSSKSTSGTAAALCLVQYFPEPTVSWNSGALTSVHTPPAVLQSS 60

QY 209 GLYSLSVVTVPSSSLGTQYICNVNHPKSTKVDKKA----- 246
 DB 61 GLYSLSVVTVPSSSLGTQYICNVNHPKSTKVDKKA----- 120

QY 247 -----EPKCDKTHCPCPAPPELGGPSVFLPPPKPDT 281
 DB 121 DTPPPCPRCPEKSCDTPPCRCPEKSCDTPPCRCPELGGPSVFLPPPKPDT 180

QY 282 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLH 341
 DB 181 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLH 240

QY 342 QDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 401
 DB 241 QDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 300

QY 402 GFPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSMHE 461
 DB 301 GFPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSMHE 360

QY 462 ALHNHYTQKSLSLSPGK 478
 DB 361 ALHNHYTQKSLSLSPGK 377

RESULT 4
 G2HU
 Ig gamma-2 chain C region - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 21-Jul-2000
 C:Accession: A93906; A92809; A90752; A93132; A02148
 J:Ellison, J.; Hood, L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
 A:Title: Linkage and sequence homology of two human immunoglobulin gamma chain con
 A:Reference number: A93906; MUID:82197621; PMID:6804948
 A:Accession: A93906
 A:Molecule type: DNA
 A:Residues: 1-326 <ELL>
 A:CROSS-references: GB:U00554; GB:J00230; NID:G22759; PIDN:CAB58438.1; PID:G6066056
 A:Note: Lys-326 is probably removed posttranslationally
 R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
 J. Immunol. 125, 1048-1054, 1980
 A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
 A:Reference number: A92809; MUID:81007873; PMID:6774012
 A:Contents: myeloma protein Til
 A:Accession: A92809
 A:Molecule type: protein
 A:Residues: 1-19, 'O', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
 A:Note: Trp-156 is at or near the complement-binding site
 R:Connell, G.E.; Parr, D.M.; Hofmann, T.
 Can. J. Biochem. 57, 758-767, 1979
 A:Title: The amino acid sequences of the three heavy chain constant region domains of a
 A:Reference number: A90752; MUID:80001357; PMID:113060
 A:Contents: myeloma protein Zie
 A:Accession: A90752
 A:Molecule type: protein
 A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
 A:Note: this sequence has since been revised
 R:Hofmann, T.; Parr, D.M.
 Mol. Immunol. 16, 923-925, 1979
 A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
 A:Reference number: A93132; MUID:80114419; PMID:118920
 A:Contents: Zie
 A:Accession: A93132

A:Molecule type: protein
 A:Residues: 239-275 <HOF>
 R:Hofmann, T.; Parr, D.M.
 submitted to the Atlas, March 1980
 A:Reference number: A94591
 A:Contents: annotation; 21e, revisions to residues 25, 59, 60, and 264-268
 A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
 ned
 R:Milstein, C.; Frangione, B.
 Biochem. J. 121, 217-225, 1971
 A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
 A:Reference number: A90283; MUID:72033500; PMID:4940472
 A:Contents: annotation; myeloma protein Sa, disulfide bonds
 R:Frangione, B.; Milstein, C.; Fink, J.R.L.
 Nature 221, 145-148, 1969
 A:Title: Structural studies of immunoglobulin G.
 A:Reference number: A93157; MUID:69064124; PMID:5782707
 A:Contents: annotation; Sa, disulfide bonds
 C:Genetics:
 A:Gene: GDB:ICHG2
 A:CROSS-references: GDB:119338; OMIM:147110
 A:Map position: 14q32.33-14q32.33
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology
 F:20-85/Domain: immunoglobulin C region; immunoglobulin homology
 F:133-202/Domain: immunoglobulin homology <IM1>
 F:239-306/Domain: immunoglobulin homology <IM2>
 F:14/Disulfide bonds: interchain (to light chain) #status experimental
 F:27-83,140-200,246-304/Disulfide bonds: #status experimental
 F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.5%; Score 1600; DB 1; Length 326;
 Best Local Similarity 90.9%; Pred. No. 1.3e-87;
 Matches 300; Conservative 12; Mismatches 14; Indels 4; Gaps 2;

QY 149 ASTKGPSVFLAPSSKSTSGTAAALCLVQYFPEPTVSWNSGALTSVHTPPAVLQSS 208
 DB 1 ASTKGPSVFLAPSSKSTSGTAAALCLVQYFPEPTVSWNSGALTSVHTPPAVLQSS 60

QY 209 GLYSLSVVTVPSSSLGTQYICNVNHPKSTKVDKKAEPKSCDKTHTCPCPAPPELLGG 268
 DB 61 GLYSLSVVTVPSSSLGTQYICNVNHPKSTKVDKKAEPKSCDKTHTCPCPAPPELLGG 116

QY 269 PSVLEPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 328
 DB 117 PSVLEPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 176

QY 329 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 388
 DB 177 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 236

QY 389 LTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 448
 DB 237 MTNQLVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 296

QY 449 QQGNVFSCSMHEALHNHYTQKSLSLSPGK 478
 DB 297 QQGNVFSCSMHEALHNHYTQKSLSLSPGK 326

RESULT 5
 G4HU
 Ig gamma-4 chain C region - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 16-Jul-1999
 C:Accession: A90933; A90249; A02150
 R:Ellison, J.; Buxbaum, J.; Hood, L.
 DNA 1, 11-18, 1981
 A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
 A:Reference number: A90933; MUID:83157104; PMID:6299662

igen Primerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'O', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A;Note: this sequence has the Gln(17) and Gln(1) markers
R;Schmidt, W.E.; Jung, H.D.; Falm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOI; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A;Note: this sequence has the Gln(3) and Gln(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) #status experimental

Query Match 68.8%; Score 1763; DB 1; Length 330;
Best Local Similarity 99.7%; Pred. No. 3e-97; Mismatches 1; Indels 0; Gaps 0;
Matches 329; Conservative 0;

Qy 149 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQSS 208
Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQSS 60

Qy 209 GLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKAEKSKDKTHTCPPCPAPELIGG 268
Db 61 GLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKAEKSKDKTHTCPPCPAPELIGG 120

Qy 269 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEOYN 328
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEOYN 180

Qy 329 STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSRDE 388
Db 181 STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSRDE 240

Qy 389 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 448
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy 449 QGQNVFSCSVMHENHVTOKSLSLSPCK 478
Db 301 QGQNVFSCSVMHENHVTOKSLSLSPCK 330

RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: con
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 63.5%; Score 1626.5; DB 2; Length 377;
Best Local Similarity 81.7%; Pred. No. 4.1e-89;
Matches 308; Conservative 10; Mismatches 12; Indels 47; Gaps 1;

Qy 149 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQSS 208
Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQSS 60

Qy 209 GLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKKA----- 246
Db 61 GLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKRELKTLPLGDTTHTCPRCPEPKSC 120

Qy 247 -----EPKSCDKTHTCPPCPAPELIGGSPVFLPPPKPKDT 281
Db 121 DTPPPCPRCPPEPKSCDTPPPCPRCPPEPKSCDTPPPCPAPELIGGSPVFLPPPKPKDT 180

Qy 282 LMTSRPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEOYNSTYRVVSVLTVLH 341
Db 181 LMTSRPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEOYNSTYRVVSVLTVLH 240

Qy 342 QDLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSRDELTKNQVSLTCLVK 401
Db 241 QDLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSRDELTKNQVSLTCLVK 300

Qy 402 GFYPDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSSVMHE 461
Db 301 GFYPDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSSVMHE 360

Qy 462 ALHNHYTOKSLSLSPCK 478
Db 361 ALHNHYTOKSLSLSPCK 377

RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 converte
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:24 ; Search time 21.453 Seconds
(without alignments)
2141.995 Million cell updates/sec

Title: US-09-758-173-8

Perfect score: 2561

Sequence: 1 MGMSLLFLFVAVTRVQCE.....MHEALHNHYTKSLSLSPGK 478

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 73.*

2: PIR1.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1763	68.8	330	1 GHU	Ig gamma-1 chain C
2	1626.5	63.5	377	2 A23511	Ig gamma-3 chain C
3	1624.5	63.4	377	2 A60764	Ig gamma-3 chain C
4	1600	62.5	326	1 G2HU	Ig gamma-2 chain C
5	1586.5	61.9	327	1 G4HU	Ig gamma-4 chain C
6	1494.5	58.4	444	2 PC4436	monoclonal antibod
7	1478	57.7	470	2 S22080	Ig heavy chain pre
8	1467.5	57.3	469	2 S37483	Ig gamma-2a chain
9	1429	55.8	472	2 S31459	Ig gamma-1 chain -
10	1415	55.3	374	2 S69339	Ig heavy chain v r
11	1415	55.3	446	2 S40295	Ig gamma-2a chain
12	1392	54.4	474	1 G2MS11	Ig gamma-2b chain
13	1338.5	52.3	475	2 S01321	Ig gamma-2b chain
14	1259	49.2	328	2 I47159	Ig gamma-2a chain
15	1256	49.0	255	4 S31866	Ig gamma-1 chain C
16	1253	48.9	328	2 I47160	Ig gamma-2b chain
17	1250	48.8	234	2 PT0207	Ig gamma chain C r
18	1247	47.9	328	2 I47158	Ig gamma-1 chain C
19	1226.5	47.9	323	1 GHRB	Ig gamma chain C r
20	1223	47.8	328	2 I47161	Ig gamma-3 chain C
21	1212.5	47.3	329	1 G2GP	Ig gamma-2 chain C
22	1157.5	45.2	308	2 C30554	Ig heavy chain C r
23	1152	45.0	289	1 G3H0W1	Ig gamma-3 heavy c
24	1148	44.8	326	2 PS0017	Ig gamma-1 chain C
25	1142.5	44.6	333	2 PS0018	Ig gamma-2b chain
26	1138	44.4	324	1 GMS	Ig gamma-1 chain C
27	1137	44.4	329	1 G3MSC	Ig gamma-3 chain C
28	1133	44.2	393	1 G1MSC	Ig gamma-1 chain C
29	1126	44.0	398	1 G3NSM	Ig gamma-3 chain C

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 16-Jul-1999

C:Accession: A93433; S3887; B90563; A90564; B91568; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers, 2

A:Note: Lys-330 is removed after translation

R:Harrie, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S3887

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <CUN>

A:Note: This sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Molecule type: protein

A:Residues: 136-154,'O',156-165,'Q',167-176,'O',178-194,'N',196-197,'D',199-238,'E',240,'

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P108593-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 8120 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-026-985-68

Query Match 78.0%; Score 1120.6; DB 3; Length 8120;
Best Local Similarity 87.5%; Pred. No. 1.6e-258;
Matches 1257; Conservative 0; Mismatches 159; Indels 21; Gaps 2;

QY 1 ATGGGTGAGGCTCATCTGTCTCTTCCTTGTCTGCTGTGCTACGGGTGTCAGTGTGAG 60
DB 1306 ATGGGATGGTCATGTATCATCTCTTTTCTAGTAGCAACTGCAACTGGAGTACATTCAGAA 1365
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DB 1366 GTTCAGCTAGTCAGTCTGGCGGTGGCTGTGTCAGGCTGGGGGTCTACTCGTTTGTCC 1425
QY 121 TGTGCACTCTCTGGATTCACCTTTCAGTACCACTACATGATTTGTTTCGCGCAGGCTCCA 180
DB 1426 TGTGCACTCTCTGGCTACTCTCTCGAGTCACTATGCACTGGGTCCGTGAGGCCCG 1485
QY 181 GGAAGGGGCGGAATGGTAGGTTTCATTAGAAACAAACCGAAGCGTGGGAGCAACAGAA 240
DB 1486 GGTAAAGGGCTGGAATGGGTGGATATATTT-----GATCCTTCCAATGGTGAACACTACG 1539
QY 241 TAGCGCGGTCTGTGAAGACAGATTCACCATCTCCAGAGATTTCCAAAGCATGCC 300
DB 1540 TATAATCAAAAGTTCAAGGGCGTTTCACTTTATCTCGGACAACTCCAAAAACACAGA 1599
QY 301 TATCTGCAATGAGCAGCTGAAATTCGAGGACAGCGCGCTTATTACTGTACTACATCC 360
DB 1600 TACCTGCAGATGAACAGCCTGCGTGTGAGGACACTGCGGTCTATTACTGTGCAAGAGG 1659
QY 361 TACATTTACATTTGCGGGGTGGTGTCTGCTATGAGGTTACTTCGAATTCGGGGCCAG 420
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QY 421 GCGGCGCTGTCACCGTCTCTCAGTAGCACCAGGGCCCATCGGTCTTCCCGCTGCA 480
DB 1705 GGAACCTGTCACCGTCTCTCTGCGGCTCCACAGAGGGCCCATCGGTCTTCCCGCTGCA 1764
QY 481 CCCTCTCTCAAGAGCAGCTCTCTGGGGGACAGCGGCGCTGGGTGCTGTCTCAAGGACTAC 540
DB 1765 CCCTCTCTCAAGAGCAGCTCTCTGGGGGACAGCGGCGCTGGGTGCTGTCTCAAGGACTAC 1824
QY 541 TTCCCGGAACCGGTGACGTTGTGGTGTGGAACCTCAGGCGGCTGACAGCGGGGTGACACAC 600
DB 1825 TTCCCGGAACCGGTGACGTTGTGGTGTGGAACCTCAGGCGGCTGACAGCGGGGTGACACAC 1884
QY 601 TTCCCGGTGCTCTACAGTCTCAGGCTCTACTCCCTCAGCAGCGGTGTCACCGTCCC 660
DB 1885 TTCCCGGTGCTCTACAGTCTCAGGCTCTACTCCCTCAGCAGCGGTGTCACCGTCCC 1944
QY 661 TCCAGCAGCTTGGGACCCAGACCTACATCTTCAACGTGAATCAAGCCCAAGCAACACC 720
DB 1945 TCTAGCAGCTTGGGACCCAGACCTACATCTGCAAGTGAATCAAGCCCAAGCAACACC 2004
QY 721 AAGGTGGAACAAGAGCAGAGGCCAAATCTTGTGACAAACTCAACATGCCCCACCGTGC 780

DB 2005 AAGGTGCAAGAAAGTTGAGCCCAAAATCTTGTGACAAAATCTCACACATGCCACCGTGC 2064
QY 781 CCAGCACCTGAACCTCTCTGGGGGACCGTCACTTCTCTTCCCGCCCAAAACCAAGGAC 840
DB 2065 CCAGCACCTGAACCTCTCTGGGGGACCGTCACTTCTCTTCTCTTCCCGCCCAAAACCAAGGAC 2124
QY 841 ACCCTATGATCTCCCGGACCCCTGAGGTGACATGCGTGTGTTGTTGACGTGACGACGACAA 900
DB 2125 ACCCTATGATCTCCCGGACCCCTGAGGTGACATGCGTGTGTTGTTGACGTGACGACGACAA 2184
QY 901 GACCTGAGGTCAAGTTCAACTGTTGAGCGGCGGTGAGGTGATATGTCACCAAGACA 960
DB 2185 GACCTGAGGTCAAGTTCAACTGTTGAGCGGCGGTGAGGTGATATGTCACCAAGACA 2244
QY 961 AAGCGCGGAGGAGCAGTACAAACAGCACGTACCGTGTGTTGTTGACGCTCTCACCGTCTCTG 1020
DB 2245 AAGCGCGGAGGAGCAGTACAAACAGCACGTACCGTGTGTTGTTGACGCTCTCACCGTCTCTG 2304
QY 1021 CACAGGACTGGGTGAATGGCAAGGAGTACAAAGTGCAGAGTCTTCCAAACAAAGCCCTCCCA 1080
DB 2305 CACAGGACTGGGTGAATGGCAAGGAGTACAAAGTGCAGAGTCTTCCAAACAAAGCCCTCCCA 2364
QY 1081 GCCCCATCGAAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACACAGGTGTAC 1140
DB 2365 GCCCCATCGAAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACACAGGTGTAC 2424
QY 1141 ACCCTGCCCATCTCCGGGATGAGTGCACCAAGAACAGGTGAGCTCAGCTCCTCGCTGGTC 1200
DB 2425 ACCCTGCCCATCTCCGGGAGAGATGACCAAGAACAGGTGAGCTCCTCGCTGGTC 2484
QY 1201 AAAGGCTTCTATCCAGCAGCATCGCGTGGAGTGGGAGCAATGGGACGCGGAGAAC 1260
DB 2485 AAAGGCTTCTATCCAGCAGCATCGCGTGGAGTGGGAGCAATGGGACGCGGAGAAC 2544
QY 1261 AACTAGAACACGAGCTCCGCTGGAGTCCGAGGCTCTTCTTCTCTACAGCAAG 1320
DB 2545 AACTAGAACACGAGCTCCGCTGGAGTCCGAGGCTCTTCTTCTCTACAGCAAG 2604
QY 1321 CTACCGTGCACAAAGAGCAGGTGGCAGCGGGGAAAGCTTCTTCTCATGCTCCGTGATGCAT 1380
DB 2605 CTACCGTGCACAAAGAGCAGGTGGCAGCGGGGAAAGCTTCTTCTCATGCTCCGTGATGCAT 2664
QY 1381 GAGGCTCTGCAACCACTACGCGAGAGAGCTCTCCCTGTCTCCGGGTAATGA 1437
DB 2665 GAGGCTCTGCAACCACTACGCGAGAGAGCTCTCCCTGTCTCCGGGTAATGA 2721

RESULT 15

US-09-121-952A-68
; Sequence 68, Application US/09121952A
; Patent No. 6458355

GENERAL INFORMATION:

; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.

TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES

; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

; ZIP: 94080

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS


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; TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
; TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
; FILE REFERENCE: 037003-0275807
; CURRENT APPLICATION NUMBER: US/09/343,485A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/023,715
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/819,866
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 18986
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: referred to as "Molly"
US-09-343-485A-2

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Query Match 78.5%; Score 1127.4; DB 4; Length 18986;
Best Local Similarity 87.8%; Pred. No. 5e-260;
Matches 1262; Conservative 0; Mismatches 151; Indels 24; Gaps 2;

Qy	1	ATGGGTGAGAGCCTCATCTTGTCTCTCTCTTGTTCGGTGTGTGCTACGCGTGTCTCAGTGTGAG	60
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Db	9493	GTAACAATCGAGAGCCTGGGGCTGAGCTGGTGAAGCTGGGGGCTCAGTGAAGATGTCTCC	9552
Qy	121	TGTGCAAGTCTCTGGATTACCTTTCAGTGACCACTACATGTATTGGTTCGCCCAAGGCTCCA	180
Db	9553	TGCAAGGCTTCTGGCTACACATTTACACAGTTTACAATATGCACTGGGTAAACACAGACACCT	9612
Qy	181	GGGAAGGGCGGGAATGGGTAGTGTTTCATTAGAAACAAACCGAACGGTGGGACAAACAGAA	240
Db	9613	GGTCTGGGGCTGGAAATGGATTGGAGCTATT-----TATCCGGAAATGGTGATATCTTCC	9666
Qy	241	TACGCCGCTCTGTGAAGACAGATTCACCATCTCCAGAGATGATTCCAAACGATCGCC	300
Db	9667	TACAATCAGAAGTTTCAAAGGCAAGGCCACATTTGCTGCAGACAAATCCTCCAGCAGAGCC	9726
Qy	301	TATCTGCAAAATCAGACAGCCTGAAAAATCGAGGACACGGCGGTCTATTACTGTACTCATCTCC	360
Db	9727	TACATGCAGCTCAGCAGCCTGCATCTCAGAGACTCTCGGCTCTATTACTGTGCAAGATC-	9785
Qy	361	TACATTTCAATTTGTGGGGTGGTGTCTGCTATAGAGGTTACTTCGAATTTCTGGGGCCAG	420
Db	9786	-----GACTTTACTACGGCGGTGACTGGTACTTTCATATGTCTGGGGCGCA	9828
Qy	421	GGGGCCCTGGTCACCGTCTCTCAGCTAGACCAAGGGCCCATCGTCTTCCCTCCCTGGCA	480
Db	9829	GGGACCACGGTCACCGTCTCTCAGCTAGCACCAAGGGCCCATCGTCTTCTCCCTCCCTGGCA	9888
Qy	481	CCCTCTCTCAAGACACCTCTGGGGGGCACAGGGCCCTGGGCTGCCCTGGTCAAGAGACTAC	540
Db	9889	CCCTCTCTCAAGACACCTCTGGGGGGCACAGGGCCCTGGGCTGCCCTGGTCAAGAGACTAC	9948
Qy	541	TTCCCCGAACCGGTGACCGTGTCTGTGGAATCTCAGCGCCCTTGACCAAGCGCGTGCACACC	600
Db	9949	TTCCCCGAACCGGTGACCGTGTCTGTGGAATCTCAGCGCCCTTGACCAAGCGCGTGCACACC	10008
Qy	601	TTTCCCGGCTGTCTTACAGTCTCAGGAATCTACTCTCCTCAGACGGTGTGTGACCGTGGCC	660
Db	10009	TTTCCCGGCTGTCTTACAGTCTCTCAGGAATCTACTCTCCTCAGACGGTGTGTGACCGTGGCC	10068
Qy	661	TCCAGCAGCTTCGGGCACCCAGACCTACATCTGCAACGTGTAATCACAGGCCCAACCAACC	720
Db	10069	TCAGCAGCTTCGGGCACCCAGACCTACATCTGCAACGTGTAATCACAGGCCCAACCAACC	10128
Qy	721	AAGGTGGACAAGAAAGACAGAGCCCAATCTTTGTGACAAAACTCACATATGCCCAACCGTGC	780

Db	10129	AAAGGTGGACAAAGAAAGACAGACCCAAATCTTGTGACAAAACTCACACATGCCACCCTGTC	10188
Qy	781	CCAGCACCTGAACTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGAC	840
Db	10189	CCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTTCCCCCAAAACCCAAAGGAC	10248
Qy	841	ACCCTCATGATCTCCGGAACCCCTGAGGTACATGTCGTGGTGGTGGACGTGAGCACGAA	900
Db	10249	ACCCTCATGATCTCCGGAACCCCTGAGGTACATGTCGTGGTGGTGGACGTGAGCACGAA	10308
Qy	901	GACCTGAGGTCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA	960
Db	10309	GACCTGAGGTCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA	10368
Qy	961	AAGCCGCGGGAGGAGCAGTCAACAGCACAGTACCGTGTGGTCAGAGGTCTCTCACCGTCTCTG	1020
Db	10369	AAGCCGCGGGAGGAGCAGTCAACAGCACAGTACCGTGTGGTCAGAGGTCTCTCACCGTCTCTG	10428
Qy	1021	CACCAAGACTGGCTGAATGCGAAGGAGTACAACTGTCAAGGTCTTCCAAACAAAGCCCTCCCA	1080
Db	10429	CACCAAGACTGGCTGAATGCGAAGGAGTACAACTGTCAAGGTCTTCCAAACAAAGCCCTCCCA	10488
Qy	1081	GCCCCCATCGAANAACCATCTCCAAAGCCAAAGGCGCCCGGAGACCCACAGGTGTAC	1140
Db	10489	GCCCCCATCGAANAACCATCTCCAAAGCCAAAGGCGCCCGGAGACCCACAGGTGTAC	10548
Qy	1141	ACCTGCCCCCATCCGGGATGAGCTGACCAAGAACAGGTGACAGCTGACCTGCCTGGTCTC	1200
Db	10549	ACCTGCCCCCATCCGGGATGAGCTGACCAAGAACAGGTGACAGCTGACCTGCCTGGTCTC	10608
Qy	1201	AAAGGCTTCTATCCACAGCAATCCGCGTGGATGGGAGAGCAATGGGAGCCGGAGAAC	1260
Db	10609	AAAGGCTTCTATCCACAGCAATCCGCGTGGATGGGAGAGCAATGGGAGCCGGAGAAC	10668
Qy	1261	AACTACAGACCAAGCCTCCCGTCTGGACTCCGACGGCTCTTCTTCTCTACAGCAAG	1320
Db	10669	AACTACAGACCAAGCCTCCCGTCTGGACTCCGACGGCTCTTCTTCTCTACAGCAAG	10728
Qy	1321	CTCACCGTGGACAAGACAGGTGGCAGCGGGGAAAGCTTCTCTCATGTCTCCGTGATGAT	1380
Db	10729	CTCACCGTGGACAAGACAGGTGGCAGCGGGGAAAGCTTCTCTCATGTCTCCGTGATGAT	10788
Qy	1381	GAGGCTCTGCACAACCACTACACGCAAGAGAGCTCTCCCTGTCTCCGGGTAATATGA	1437
Db	10789	GAGGCTCTGCACAACCACTACACGCAAGAGAGCTCTCCCTGTCTCCGGGTAATATGA	10845

RESULT 13

US-09-027-449-68

; Sequence 68, Application No. 6025158

; FACILE NO. 6023138
; GENERAL INFORMATION:

APPLICANT: Gonzalez, Tania R.

APPLICANT: Leong, Steven R.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and

;	TITLE OF INVENTION:	Hum
:	NUMBER OF SEQUENCES:	72

; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San F

STATE: Calif

; COUNTRY: U

; ZIP: 94080
; COMPUTER READABLE FORM.

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 5 inch 1 44 Mb floppy disk

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; MEDIUM TYPE: 3.5 INCH, 1.44
 ; COMPUTER: IBM PC compatible

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; IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: WinPatIn (Ge...

; CURRENT APPLICATION DATA:

Query Match	78.5%;	Score 1127.4;	DB 4;	Length 9209;
Best Local Similarity	87.8%;	Pred. No. 4.1e-260;		
Matches 1262;	Conservative	0;	Mismatches 151;	Indels 24; Gaps
QY	1	ATCGGTTGGAGCCTCATCTTGCTTCTCTCTGTCGCTGTGCTACGCGTGCACGTGAG	60	
Db	2401	ATGGGTTGGAGCCTCATCTTGCTTCTCTCTGTCGCTGTGCTACGCGTGCCTGTCCAG	2460	
QY	61	GTCCAACTGGTGGAGTCTGGGGAGGCTTGGTGCACGCTCGCGGTCCCTGAGAGTCTCC	120	
Db	2461	GTACAACTGCAGCAGCCTGGGCTGAGCTGTGTGAAGCCTCGGGGCTCAGTCAAGATGTC	2520	
QY	121	TGTGCAGTCTCTGGATTACCTTTCAGTGACCACTACATGTATTGGTTCGCGCAGCTCCA	180	
Db	2521	TGCAAGGCTCTTGGCTACACATTTACAGTTTACAATATGCACTGGGTAAACAGACACT	2580	
QY	181	GGGAAGGCGCGGAATGGGTAGTGTTCATTAGAAACAAACCGAAGCGGTGGGACACAGAA	240	
Db	2581	GGTCGGGGCTTGGATGGATTGGAGCTATT-----TATCCGGAAATGGTGATACTTCC	2634	
QY	241	TACGCGCGCTCTGTGAAGACAGATTACCATCTCCAGAGATGATTCGAAAGGATCGCC	300	
Db	2635	TACATCAAGATTTCAAAGGCAAGGCCACATTGACTGCAGACAATCCTCCAGCAGACC	2694	
QY	301	TATCTGCAAAATGAGCAGCCTGAAAATCGAGGACACGGCGCTCTATTACTGTACTTACATCC	360	
Db	2695	TACATCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATC-	2753	
QY	361	TACATTTACATTTGCGGGTGGTGTGCTATGAGGTTACTTCGAAATTCCTGGGGCCAG	420	
Db	2754	-----GACTTACTACGGCGGTGACTGTACTTCAATGTCTGGGGCGCA	2796	
QY	421	GGCGGCTTGGTCAACCGTCTCTCAGCTAGCACCAAGGGGCCCATCGGTCTTCCCGCTGGCA	480	
Db	2797	GGGACCACGGTCAACCGTCTCTGAGCTAGCACCAAGGGGCCCATCGGTCTTCCCGCTGGCA	2856	
QY	481	CCCTCTCCAAGACACCTCTCGGGGCAACGCGGCCCTGGGCTCCCTGGTCAAGGACTAC	540	

[illegible]

Db	1109	GCCCCATCGAGNAACATCTCCAAAGGCCAGCCCCGAGAACACACAGGTGAC	1161
Qy	1141	ACCTGCCCCCATCCCGGATGAGTGCACCAAGAACAGTTCAGCTGACCTGCTCGTC	1200
Db	1169	ACCTGCCCCCATCCCGGATGAGTGCACCAAGAACAGTTCAGCTGACCTGCTCGTC	1228
Qy	1201	AAAGGCTTCTATCCCAAGCACATCCCGTGGAGTGGGAGAGCAATGGCAGCCGAGAAC	1260
Db	1229	AAAGGCTTCTATCCCAAGCACATCCCGTGGAGTGGGAGAGCAATGGCAGCCGAGAAC	1288
Qy	1261	AACTACAAGACCAACGCTCCCGTGTGGACTCCGACGCTCTTCTTCTCTACAGCAAG	1320
Db	1289	AACTACAAGACCAACGCTCCCGTGTGGACTCCGACGCTCTTCTTCTCTACAGCAAG	1348
Qy	1321	CTCAGCTGGACAAAGACAGTGGCAGCAGGGGACGCTTCTCATGCTCCGTGATGCAT	1380
Db	1349	CTCAGCTGGACAAAGACAGTGGCAGCAGGGGACGCTTCTCATGCTCCGTGATGCAT	1408
Qy	1381	GAGGCTCTGCACAACCACTACACGACGAGAGGCCTCTCCCTGTCTCCGGTAAATGA	1437
Db	1409	GAGGCTCTGCACAACCACTACACGACGAGAGGCCTCTCCCTGTCTCCGGTAAATGA	1465

RESULT 6

US-08-149-099C-3
; Sequence 3, Application US/08149099C
; Patent No. 5736137
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, Darrell R.
; APPLICANT: HANNA, Nabil
; APPLICANT: LEONARD, John E.
; APPLICANT: NEWMAN, Roland A.
; APPLICANT: REFF, Mitchell E.
; APPLICANT: RASTETTER, William H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
; TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
; TITLE OF INVENTION: LYMPHOMA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,099C
; FILING DATE: 03-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 12-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9209 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

Qy	149	ACC	ACTACATG	TATTTGGTTC	CGCAGGCT	CCAGGAAGGGCCGGAAATGGGTAGT	TTCA	205
Db	133	GCA	ATTCTAT	TCATCTGGGTC	CGCCAGGCT	CCAGCAAGGGGTGGAGTGGGTGGCAGTTA		192
Qy	209	TTAGAAA	CAAAAC	CGAACGGTGGGACAACAGATACGCGCGCTCTGTGAAGACACAGATTCA				268
Db	193	TATTATATGATGGAAATCAT	-----	AAATTCTACGAGACTCCGTTGAAGGGCCGATTCA				246
Qy	269	CCATCTCCAGAGATGATTTCCAAAGCATTCGCTATCTGCAAAATGAGCAGCCTGGAATAATCG						328
Db	247	CCATTTCAGAGACAATTTCCAAGAACACACTGTATCTGGAAGTGAAGAGCCTTGCAAACTG						306
Qy	329	AGGACACGGCCGCTCTATTACTGTACTACATCTCTACATTTTCACATTTGTCGGGGTGTGTCT						388
Db	307	AGGACACGGGTGCTCTATTATCTGTATAGAGATCAAACT	-----	-----	-----	-----	-----	345
Qy	389	GCTATGGAGGTTACTTCGAAATTTCTGGGGCCAGGGCGCCCTGTGTCACTCTCTCTCAGCTA						448
Db	346	ACGGAGTCCAAGATTTGCACTCTCTGGGGCCAGGAAACCTTGTTCACTCTCTCTCAGCT						405
Qy	449	GCACCAAGGGCCCATCGGTCTTCCCTCTGGCACCTCTCTCCAGAGACACTCTGTGGGGCA						508
Db	406	CCACCAAGGGCCCATCGGTCTTCCCTCTGGCACCTCTCTCCAGAGACACTCTGTGGGGCA						465
Qy	509	CAGCGGCTTGGGTGCTTGTTCAAGGACTACTTCCCTCCGAAACCGGTGACGGTGTGGTGA						568
Db	466	CAGCGGCTTGGGTGCTTGTTCAAGGACTACTTCCCTCCGAAACCGGTGACGGTGTGGTGA						525
Qy	569	ACTCAGGGCCCTGACACAGCGGGTGGACACTTTCGGGCTGTCTTACGTCTCTCAGNAC						628
Db	526	ACTCAGGGCCCTTGGCCAGCGGGTGGACACTTTCGGGCTGTCTTACAGTCTCTCAGNAC						585
Qy	629	TCTACTCTCTCAGCAGCGTGGTGACCGTGCCTCTCAGCAGCTTGGGCACCCAGACCTACA						688
Db	586	TCTACTCTCTCAGCAGCGTGGTGACCGTGCCTCTCAGCAGCTTGGGCACCCAGACCTACA						645
Qy	689	TCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGACCAAGAAAGCAGAGCCCAAT						748
Db	646	TCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGACCAAGAAAGTGAAGCCCAAT						705
Qy	749	CTTGTGACAAATCTCACATGCCACCGTGCCACGACTGAACTCTCTGGGGGACCGT						808
Db	706	CTTGTGACAAATCTCACATGCCACCGTGCCACGACTGAACTCTCTGGGGGACCGT						765
Qy	809	CAGCTTCTCTTCCCCCCCCAAACCCAAAGGACACCTCTATGATCTCCGGAGCCCTGAGG						868
Db	766	CAGCTTCTCTTCCCCCCCCAAACCCAAAGGACACCTCTATGATCTCCGGAGCCCTGAGG						825
Qy	869	TCACATCGTGGTGGAGTGGAGCCAGAGACCCCTGAGTCAAGTTCAACTGGTACG						928
Db	826	TCACATCGTGGTGGAGTGGAGCCAGAGACCCCTGAGTCAAGTTCAACTGGTACG						885
Qy	929	TGGAACGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACAAACGCA						988
Db	886	TGGAACGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACAAACGCA						945
Qy	989	CGTACCGTGTGGTCAGCGTCTCTACCGTCTTGACACGAGACTGGCTGTAATGSCAAGAGT						1048
Db	946	CGTACCGGGTGTGACGCTCTTCCACCTCTTGACACGAGACTGGTGTGTAATGSCAAGAGT						1005
Qy	1049	ACAAAGTCAAAAGGTTCTCAACAAAGAGCCCTCCACGCCCCCATCGAGAAAACCACTCCCAAG						1108
Db	1006	ACAAAGTCAAAAGGTTCTCAACAAAGAGCCCTCCACGCCCCCATCGAGAAAACCACTCCCAAG						1065
Qy	1109	CCAAAGGGCAGCCCCCGAGAACCAAGGTGTACACCTTGCCCCCATCCCGGGATGAGCTGA						1168
Db	1066	CCAAAGGGCAGCCCCCGAGAACCAAGGTGTACACCTTGCCCCCATCCCGGGATGAGCTGA						1125
Qy	1169	CCAAGAACCAAGGTCAGCCTTGACCTGCTGTCAAAAGGCTTCTATCCAGGCACATCGCCG						1228
Db	1126	CCAAGAACCAAGGTCAGCCTTGACCTGCTGTCAAAAGGCTTCTATCCAGGCACATCGCCG						1185
Qy	1229	TGGAGTGGGAGACAAATGGGGCAGCCGGAGAAACAACTTACAAGAACCAACGCTCCGCTGCTGG						1288

Db	1186	TGGAGTGGGAGAGCAATGGGACGGGAGAACTACAAGACCAACGCTCCCGTGTCTGG	1245
Qy	1289	ACTCCGACGGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAGAGAGGTGGCAGC	1348
Db	1246	ACTCCGACGGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAGAGAGGTGGCAGC	1305
Qy	1349	AGGGAAACGTCTTCTCATGTCCTCGTGATCATGAGGCTCTGCACAACCACTACACGAGA	1408
Db	1306	AGGGAAACGTCTTCTCATGTCCTCGTGATCATGAGGCTCTGCACAACCACTACACGAGA	1365
Qy	1409	AGAGCCCTCCCTGTCTCCGGGTAAATGA	1437
Db	1366	AGAGCCCTCCCTGTCTCCGGGTAAATGA	1394
RESULT 4			
US-08-157-101A-9			
; Sequence 9, Application US/08157101A			
; Patent No. 5808032			
; GENERAL INFORMATION:			
; APPLICANT: KURIHARA, TATSUYA			
; APPLICANT: MATSUKURA, SHIGEKAZU			
; APPLICANT: TSURUOKA, NOBUO			
; APPLICANT: ARIMA, KENJI			
; APPLICANT: NISHIHARA, TATSURO			
; TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION			
; TITLE OF INVENTION: PLASMIDS THEREFOR			
; NUMBER OF SEQUENCES: 9			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: PILLSBURY, MADISON & SUTRO			
; STREET: 1100 NEW YORK AVENUE, N.W.			
; CITY: WASHINGTON			
; STATE: D.C.			
; COUNTRY: USA			
; ZIP: 20005			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC Compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent in Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/157.101A			
; FILING DATE: 05-APR-1994			
; CLASSIFICATION: 530			
; ATTORNEY/AGENT INFORMATION:			
; NAME: TITUS, MARLANA K			
; REGISTRATION NUMBER: 35843			
; REFERENCE/DOCKET NUMBER: 9437/204199			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 202-861-3711			
; TELEFAX: 202-822-0944			
; TELEX: 6714627 CUCH			
; INFORMATION FOR SEQ ID NO: 9:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1350 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: DNA (genomic)			
US-08-157-101A-9			
Query Match 79.5%; Score 1142; DB 1; Length 1350;			
Best Local Similarity 90.8%; Pred. No. 7, 7e-264;			
Matches 1249; Conservative 0; Mismatches 100; Indels 27; Gaps			
Qy	59	AGTGCNACTGGTGGAGCTGGGGAGCGCTGGTCCAGCCTGGCGGGTCCCTGAGACTCT	118
Db	2	AGGTGCAGCTGGTGGAGCTGGGGAGGCGGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT	61
Qy	119	CTGTGCAGTCTCTGGATTTCACCTTCAGTGCACCACTACATGATTGGTTCGCGCAGGCTC	178
Db	62	CTGTGCAGCTCTGATTCACCTTCAGTGCACCACTACATGATTGGTTCGCGCAGGCTC	121

Db 9616 GCTCCAGGCGAGGGCTGGAGTGGTCTCACGTATTAGTA-----GTAGTGGTATCCC 9669
Qy 235 ACAGATACCGCGCTGTGTAAGACAGATTACCATCTCCAGAGATGATTCCTCAAGAGC 294
Db 9670 ACATGTGACGACACTCCGTGTAAGGCGAGATTACCATCTCCAGAGAGAACCCCAAGAAC 9729
Qy 295 ATGCGCTATCTGCAATATGACGACCTGAAATTCAGAGACACGCGCGCTCTATTACTGTACT 354
Db 9730 ACATGTTCTTCAATGAACAGCCTGAGCTGAGGACACGCGCTGTCTATTACTGTGCG 9789
Qy 355 ACATCTCATATTTCAATTGTGCGGGTGTGTCTGCTATGAGAGTTACTTTCGAATTCGG 414
Db 9790 AGCT-----TGACTACAGGCTCTGACTCCCTGG 9817
Qy 415 GGCAGGCGCCCTGTCTACCGTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCC 474
Db 9818 GGCAGGAGTCTGTGTACCGTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCC 9877
Qy 475 CTGGCACCTCTCTCAAGAGACCTCTGGGGGCAACGCGGCCCTGGGCTGCTGTGCTCAAG 534
Db 9878 CTGGCACCTCTCTCAAGAGACCTCTGGGGGCAACGCGGCCCTGGGCTGCTGTGCTCAAG 9937
Qy 535 GACTACTTCCCGAAACCGGTGACGCTGTGTGGAATCTCAGGCGCCCTGACAGCGCGCTG 594
Db 9938 GACTACTTCCCGAAACCGGTGACGCTGTGTGGAATCTCAGGCGCCCTGACAGCGCGCTG 9997
Qy 595 CACACTTCCCGGCTGCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACC 654
Db 9998 CACACTTCCCGGCTGCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACC 10057
Qy 655 GTGCGCTTCCAGAGCTTGGGCAACCCAGACCTACATCTGCAACGTGGAATCACAGCCACG 714
Db 10058 GTGCGCTTCCAGAGCTTGGGCAACCCAGACCTACATCTGCAACGTGGAATCACAGCCACG 10117
Qy 715 AACCAAGGTGACAAAGAACAGAGCCCAATCTTGTGAACAACTCACACATGCCCA 774
Db 10118 AACCAAGGTGACAAAGAACAGAGCCCAATCTTGTGAACAACTCACACATGCCCA 10177
Qy 775 CCGTGCCAGCACTGAATCTTGGGGGACGCTCAGTCTTCTCTTCCCGCCCAAAACCC 834
Db 10178 CCGTGCCAGCACTGAATCTTGGGGGACGCTCAGTCTTCTCTTCCCGCCCAAAACCC 10237
Qy 835 AAGACACCTCTATGATCTCCCGGACCCCTGAGGTCACTGCGTGTGTGGACGTGAC 894
Db 10238 AAGACACCTCTATGATCTCCCGGACCCCTGAGGTCACTGCGTGTGTGGACGTGAC 10297
Qy 895 CACGAAGCCTGAGTCAAGTTCAACTGGTACGTGACGCGCTGAGGTGCATATGCC 954
Db 10298 CACGAAGCCTGAGTCAAGTTCAACTGGTACGTGACGCGCTGAGGTGCATATGCC 10357
Qy 955 AAGACAAAGCGGGAGGAGCAGTACAAACAGCAGTACCGTGTGTGTCAGCGTCTTACC 1014
Db 10358 AAGACAAAGCGGGAGGAGCAGTACAAACAGCAGTACCGTGTGTGTCAGCGTCTTACC 10417
Qy 1015 GTCTGCAACGAGACTGGCTGAATGGAAGAGGTACAAAGTGCAGAGTCTTCAACAAAGCC 1074
Db 10418 GTCTGCAACGAGACTGGCTGAATGGAAGAGGTACAAAGTGCAGAGTCTTCAACAAAGCC 10477
Qy 1075 CTCCAGCGCCCATCGAGAAACCATCTTCAAGCCAAAGGGGAGCGCCCGAGAACACACAG 1134
Db 10478 CTCCAGCGCCCATCGAGAAACCATCTTCAAGCCAAAGGGGAGCGCCCGAGAACACACAG 10537
Qy 1135 GTGTACACCTTCCCGCCCATCTCCGGGATGAGTACCAAGAACACAGGTGACCTGACTGC 1194
Db 10538 GTGTACACCTTCCCGCCCATCTCCGGGATGAGTACCAAGAACACAGGTGACCTGACTGC 10597
Qy 1195 CTGCTCAAGAGCTTCTATCCAGCAGCATCCCGTGGAGTGGGAGAGCAATGGCGAGCCG 1254
Db 10598 CTGCTCAAGAGCTTCTATCCAGCAGCATCCCGTGGAGTGGGAGAGCAATGGCGAGCCG 10657
Qy 1255 GAGAACAACTACAGACCAACGCTTCCCGTGTGAGTCCGACCGCTCTTCTTCTCTCTAC 1314

Db 10658 GAGAACAACTACAGACCAACGCTCCCGTGTGAGCTCCGACGGCTCTTCTTCTCTAC 10717
Qy 1315 AGCAAGCTACCGTGGGACAAAGACAGAGTGCACAGAGGGAACGTCTTCTCATGCTCGTG 1374
Db 10718 AGCAAGCTACCGTGGGACAAAGACAGAGTGCACAGAGGGAACGTCTTCTCATGCTCGTG 10777
Qy 1375 ATGATGAGGCTGTGCAACCACTACACAGAGGCTCTCCCTGTCTCCGGGTAAA 1434
Db 10778 ATGATGAGGCTGTGCAACCACTACACAGAGGCTCTCCCTGTCTCCGGGTAAA 10837
Qy 1435 TGA 1437
Db 10838 TGA 10840

RESULT 3
US-08-157-101A-6
; Sequence 6, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1576 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-157-101A-6

Query Match 80.4%; Score 1155.8; DB 1; Length 1576;
Best Local Similarity 90.1%; Pred. No. 4.1e-267;
Matches 1270; Conservative 0; Mismatches 112; Indels 27; Gaps 2;

Qy 29 TTGTGCTGTTGTACGGGTGTCCAGTGTGAGGTGCACACTGTGGAGTCTGGGGAGGCT 88
Db 13 TCGTTGGCCTTTAAGAGGTGTCCAGTGTCCAGTGTGAGTCTGGGAGGCG 72
Qy 89 TGGTCCAGCCTGGCGGTCCTGTGAGTGTCTCTGTGCAAGTCTCTGGATTACCTTCAGTG 148
Db 73 TGGTCCAGCCTGGGAGGTCCCTGTGAGACTCTCTGTGCAAGCCTCTGGATTACCTTCAGTA 132

Best Local Similarity 100.0%; Pred. No. 0;		Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	ATGGGTTGGAGCCTCATCTTGCTCTTCTTGTGCTGTGTGTAGCGGTGTCAGGTGTGAG	60
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Qy	181	GGGAAGGGCCGGAATGGGTAGGTTTCATTAGAAACAAACCGATGGGACACAGAA	240
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Qy	301	TATCTGCAATGAGCAGCCTGAAATCGAGGACACGGCGCTATTACTGTACTACATCC	360
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Qy	421	GGCGCCTCGTCAACGCTCTCCTCAGTACACCAAGGGCCCATCGGTCTTCCCGCTGGCA	480
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Qy	481	CCCTCTCTCAAGAGCACCTCTGGGGGCAACAGCGCCCTGGGCTGCTGGTCAAGCACTAC	540
Db	481	CCCTCTCTCAAGAGCACCTCTGGGGGCAACAGCGCCCTGGGCTGCTGGTCAAGCACTAC	540
Qy	541	TTCCCGGAAACCGGTGACGCTGTGTGGAACCTCAGGGCCCTGACAGGGCGGTGACACC	600
Db	541	TTCCCGGAAACCGGTGACGCTGTGTGGAACCTCAGGGCCCTGACAGGGCGGTGACACC	600
Qy	601	TTCCCGGCTGTCTCAGTCTCCTCAGGACTCTACTCCTCAGCAGCGTGTGACCGTGCC	660
Db	601	TTCCCGGCTGTCTCAGTCTCCTCAGGACTCTACTCCTCAGCAGCGTGTGACCGTGCC	660
Qy	661	TCCAGCAGCTTGGGCAACCCAGACCTACATCTGCAAGCTGAATCAACAGCCCAACACC	720
Db	661	TCCAGCAGCTTGGGCAACCCAGACCTACATCTGCAAGCTGAATCAACAGCCCAACACC	720
Qy	721	AGGTTGCAAGAAACAGAGCCCAATCTTGTGACAAACTCACACATGCCCAACCGTGC	780
Db	721	AGGTTGCAAGAAACAGAGCCCAATCTTGTGACAAACTCACACATGCCCAACCGTGC	780
Qy	781	CCAGCACCTGAACTCTGGGGGAGCGTCACTCTTCTTCCCGCCAAACCAAGGAC	840
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Qy	841	ACCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGAGCGTGAACCCAGAA	900
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Qy	901	GACCTGAGGTCAAGTTCAACTGAGTACGTGGACCGGCTGAGGTGCAATGCCAAGACA	960
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Db	1021	CACGAGACTTGGCTGAATGGCAAGGAGTCAAGTGAAGGTCTTCCAAACCAAGCCCTCCA	1080
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Qy	1201	AAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGAGCGGAGAAC	1260
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Qy	1321	CTCACCTGGACAAAGACAGGTGGCAGCAGGGGAAACGTTTCTCATGTCTCCGTGATCAT	1380
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Qy	1381	GAGGCTCTGCACAAACCACTACACGAGAGAGGCTCTCCCTGTCTCCGGTAAATGA	1437
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RESULT 2
US-09-343-485A-3
; Sequence 3, Application US/09343485A
; Patent No. 6413777
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL R.
; APPLICANT: BARNETT, RICHARD S.
; APPLICANT: MCLACHLAN, KAREN S.
; TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
; TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
; FILE REFERENCE: 037003-0275807
; CURRENT APPLICATION NUMBER: US/09/343,485A
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/023,715
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/819,866
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 19040
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: referred to as "Mandy"
US-09-343-485A-3

Query Match 82.0%; Score 1177.8; DB 4; Length 19040;
Best Local Similarity 90.6%; Pred. No. 4.5e-272;
Matches 1307; Conservative 0; Mismatches 92; Indels 44; Gaps 3;

Qy	1	ATGGGTTGGAGCCTCATCTTGTGCTCTTGTGCTGTGTGCTACGCGTGTCCAGGTGTGAG	60
Db	9436	ATGGGTTGGAGCCTCATCTTGTGCTCTTGTGCTGTGTGCTACGCGTGTCTGTCGAG	9495
Qy	61	GTGCAACTGGTGGAGTCTGGGGAGGCTTGGTTCAGCTGCGGGTCCCTGAGAGTCTCC	120
Db	9496	GTGCAAGTGGTGGAGTCTGGGGAGGCTTGGCAAGGCTCGGGGGTCCCTGAGACTCTCC	9555
Qy	121	TGTGAGTCTCTG-----GATTACCTTCAGTGACCACTACATGTATTGTTCCGCGCAG	174
Db	9556	TGCGCAGCTCCCGGGTTCAGGTTTCCCTTCAATAACTACTACATGAGTGGTCCGCGCAG	9615
Qy	175	GCTCCAGGAAGGGCGCGGAATGGTAGGTTTTCATTAGAAAAACCAACCGGATGGGACA	234

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:47:34 ; Search time 65.4298 Seconds
(without alignments)
6735.375 Million cell updates/sec

Title: US-09-758-173-7
Perfect score: 1437
Sequence: 1 ATGGGTGAGGCTCATCTT.....CCTGCTCTCCGGGTAATGA 1437

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
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4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/prodata/1/ina/PCUTS_COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1437	100.0	1437	3	US-08-487-550-7
2	1177.8	82.0	19040	4	US-09-343-485A-3
3	1155.8	80.4	1576	1	US-08-157-101A-6
4	1142	79.5	1350	1	US-08-157-101A-9
5	1131.8	78.8	1617	2	US-08-378-939-9
6	1127.4	78.5	9209	1	US-08-149-099C-3
7	1127.4	78.5	9209	1	US-08-476-275-2
8	1127.4	78.5	9209	2	US-08-478-967A-3
9	1127.4	78.5	9209	2	US-08-475-815B-3
10	1127.4	78.5	18986	2	US-08-819-866-2
11	1127.4	78.5	18986	2	US-09-023-715-2
12	1127.4	78.5	18986	4	US-09-343-485A-2
13	1120.6	78.0	8120	3	US-09-027-449-68
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16	1118.2	77.8	8120	4	US-09-234-340A-68
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20	1118.2	77.8	1428	2	US-08-634-400-19
21	1118.2	77.8	1428	2	US-08-635-878-19
22	1118.2	77.8	1428	2	US-08-770-057-19
23	1118.2	77.8	1428	4	US-09-335-697B-19
24	1118.2	77.8	1428	4	US-09-335-697B-19
25	1117.2	77.5	1431	3	US-08-487-550-3
26	1113.4	77.5	1428	1	US-08-488-376-17
27	1113.4	77.5	1428	2	US-08-634-223-17

Query Match 100.0%; Score 1437; DB 3; Length 1437;

ALIGNMENTS

RESULT 1
US-08-487-550-7
; Sequence 7, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1437 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1437
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1437
; US-08-487-550-7

Sequence 17, Appl
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Sequence 11, Appl
Sequence 7, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 17, Appl
Sequence 21, Appl
Sequence 42, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 49, Appl
Sequence 49, Appl

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29 1113.4 77.5 1428 2 US-08-634-400-17
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31 1113.4 77.5 1428 2 US-08-770-057-17
32 1113.4 77.5 1428 4 US-09-335-697B-17
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34 1112.4 77.4 1431 3 US-08-487-550-11
35 1108 77.1 1418 4 US-08-793-450-7
36 1102 76.7 6557 1 US-08-286-740-3
37 1102 76.7 6557 5 PCT-US95-09576-3
38 1087 75.6 1567 3 US-09-049-672A-17
39 1079 75.1 1655 3 US-09-049-672A-21
40 1036.6 72.1 1329 5 PCT-US96-13152-3
41 1021.8 71.1 7731 4 US-09-301-593-42
42 1021.4 71.1 1135 1 US-08-236-311-8
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44 1021.4 71.1 6285 1 US-08-457-420A-49
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DB 523 TTCCCGAACCGGTGACGGTGTCTGGAAGCTCAGGCGCCCTGACAGCGCGGTGCACACC 582
QY 601 TTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCC 660
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DB 643 TCAGAGAGCTTGGGACCCAGACTACATCTGCAAGCTGAATCAGCCCAAGCAACACC 702
QY 721 AAGGTGACAAAGAACGAGCCCAATCTTGCAAAAGCTACACATGCCCAACCGTGC 780
DB 703 AAGGTGACAAAGAACGAGCCCAATCTTGCAAAAGCTACACATGCCCAACCGTGC 762
QY 781 CAGACCTGAACTCTGGGGGACCGTCAAGTCTTCTTCTTCCCCCAAAACCAAGGAC 840
DB 763 CAGACCTGAACTCTGGGGGACCGTCAAGTCTTCTTCTTCCCCCAAAACCAAGGAC 822
QY 841 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGAGCGTGAAGCAAG 900
DB 823 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGAGCGTGAAGCAAG 882
QY 901 GACCTGAGGTCAAGTTCAACTGGTACGTGACGGCGGTGGAGGTGCATAATGCCAAGACA 960
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QY 1081 GCGCCCATCGAAGAACCATCTTCCAAAGCCAAAGGCGAGCCCGAGAACCCACAGGTGTAC 1140
DB 1063 GCGCCCATCGAAGAACCATCTTCCAAAGCCAAAGGCGAGCCCGAGAACCCACAGGTGTAC 1122
QY 1141 ACCCTGCCCCCATCCCGGATGAGCTGACCAAGACCAAGGTGAGCTGACCTGCTGGTGC 1200
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QY 1381 GAGGCTCTGCAACACCTACACGAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1437
DB 1363 GAGGCTCTGCAACACCTACACGAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1419

RESULT 15
AAC84208
ID AAC84208 standard; DNA; 1442 BP.
XX
AC AAC84208;
XX
DT 19-MAR-2001 (first entry)
XX
DE Plasmid Lambda-1Bpcd DNA sequence.
XX
KW Monoclonal antibody; F protein; respiratory syncytial virus; RSV;
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KW
XX
OS
XX
PN WO200069462-A1.
XX
PD 23-NOV-2000.
XX
PF 18-MAY-2000; 2000MO-US13694.
XX
PR 18-MAY-1999; 99US-0134702.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Gross MS, Sweet RW, Taylor G;
XX
XX WPI; 2001-024947/03.
DR
XX
XX Human monoclonal antibody and functional fragments, useful for
PT therapeutic and/or prophylactic treatment of respiratory syncytial
PT virus infection, is specifically reactive with the F protein epitope of
PT the virus -
XX
XX Claim 3, 6; Fig 10A-B; 102pp; English.
XX
XX The invention provides a human monoclonal antibody (I) and its functional
CC fragments specifically reactive with an F protein epitope of respiratory
CC syncytial virus (RSV), and capable of neutralizing infection by the virus
CC such as Lambda-1A or Lambda-1B. The antibody can be expressed by
CC standard recombinant methodology. (I) is useful for detecting RSV by
CC contacting a source suspected of containing RSV with (I) and determining
CC whether (I) binds to the source. (I) is also useful for providing passive
CC immunotherapy prophylactically, to RSV disease in a human. (I) is useful
CC for therapeutic and/or prophylactic treatment of RSV infection in human
CC patients, particularly infants and young children. (I) is also useful
CC as a diagnostic reagent for the determination of RSV mediated disorders
CC or for tracking progress of treatment of the disorders. The present
CC sequence represents the continuous DNA sequence of the coding region of
CC the heavy chain of plasmid Lambda-1Bpcd.
XX
SQ Sequence 1442 BP; 335 A; 458 C; 388 G; 261 T; 0 other;

Query Match 81.4%; Score 1169.4; DB 22; Length 1442;
Best Local Similarity 90.2%; Pred. No. 3.1e-224;
Matches 1296; Conservative 0; Mismatches 111; Indels 30; Gaps 3;

QY 1 ATGGGTTGAGCGCTCATCTTGCTCTTCCTTGTCTGCTGTTGCTACGCGTGTCCAGTGTGAG 60
DB 27 ATGGGATGGAGCTGTATCATCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACATCCGAG 86
QY 61 GTGCAACTGGTGGAGTCTGGGGAGGCTTGGTCCAGCTGGCGGTCCCTGAGAGTCTCC 120
DB 87 GTGCACTGGTGGAGTCTGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGAGACTCTCC 146
QY 121 TGTGCACTCTCTGGATTACCTTTCAGTGCACCTACATGTTATTTGGTTCGCCAGGCTCCA 180
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DB 207 GGGAGGGGCTGGAAATGGGTCTCTTCCATT-----ACTGGTATGATGAATATACATACAC 260
QY 241 TAGCGCGCTCTGTGAAAGACAGATTTCACCATCTCCAGAGATGATTCCTCAAGAGCATCGCC 300
DB 261 TACTCAGACTCAGTGAAGGCGGATTCACCATCTCCAGAGACACGCCATGAATCACTG 320
QY 301 TATCTGCAATCAGCAGCTGAAATTCGAGGACACGGCGCTTATTACTGTACTACATCC 360
DB 321 TATCTGCAATGAACAGCTGACAGCGCTGACAGCGGAGACAGGGTGTATTATTGTGCGACA--- 377
QY 361 TACATTTACATTTGCGGGTGGTGTCTGCTATGAGGTTACTTCGAATTTCTGGGGCCAG 420
DB 378 -----CAACCGGGGAGCTGGCGCT-----TTTGACCATTTGGGGCCAG 416
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QY 1381 GAGGCTCTGCACAACTACACGACAGAGAGGCTCTCCCTCTCTCCGGTAAATGA 1437
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 Db 1472 GAGGCTCTGCACAACTACACGACAGAGAGGCTCTCCCTCTCTCCGGTAAATGA 1528
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RESULT 11
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 ID AAV61794 standard; DNA; 19035 BP.
 XX AC AAV61794;
 XX DT 07-JUN-1999 (first entry)
 XX Traget plasmid Mandy containing anti-CD23 gene.

DE Mandy; target plasmid; gene integration; gene amplification;
 XX homologous recombination; vector; neomycin phosphotransferase;
 KW neo gene; selectable marker; immunoglobulin; CD23; 5E8; human; ss.
 XX

OS Chimeric - Mus sp.
 OS Chimeric - Escherichia coli.
 OS Chimeric - Baculovirus.
 OS Chimeric - Cytomegalovirus.
 OS Chimeric - Rhesus macaque polyoma virus.
 OS Chimeric - Photinus sp.
 OS Chimeric - Salmonella typhimurium.
 OS Chimeric - Homo sapiens.

XX

FH Key Location/Qualifiers
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 FT /note= "this base represents a nucleotide missing
 from the sequence given in the
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 maintain the nucleotide numbering in the
 specification for this sequence"

FT misc_feature 721
 FT /tag= b
 FT /note= "this base represents a nucleotide missing
 from the sequence given in the
 specification. It is included to
 maintain the nucleotide numbering in the
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FT misc_feature 2941
 FT /tag= c
 FT /note= "this base represents a nucleotide missing
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 maintain the nucleotide numbering in the
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FT misc_feature 3301
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FT misc_feature 4261
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FT misc_feature 4621..4622
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FT misc_feature 8161
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FT misc_feature 8521..8522
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FT misc_feature 14641..14642
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FT misc_feature 15001..15002
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FT misc_feature 15961..15962
 FT /tag= n
 FT /note= "these bases represent nucleotides missing
 from the sequence given in the
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 maintain the nucleotide numbering in the
 specification for this sequence"

FT misc_feature 16321..16322
 FT /tag= o
 FT /note= "these bases represent nucleotides missing
 from the sequence given in the
 specification. They are included to
 maintain the nucleotide numbering in the
 specification for this sequence"

PN WO9841645-A1.
 XX 24-SEP-1998.
 XX 09-MAR-1998;
 XX 98WO-US03935.
 XX 13-FEB-1998;
 PR 98US-0023715.
 XX 14-MAR-1997;
 XX 97US-0819866.
 PA (IDEC-) IDEC PHARM CORP.

QY 121 TGTGAGTCTCTGATTCACCTTTCAGTGACCACTACATGTTATGTTTCGCCAGGCTCA 180
Db 124 TGTGAGCTCTTGATTCACCTTTAGCACTATGCGATGGTTCGCCAGGCTCA 183
QY 181 GGAAGGGGCGGAAATGGGTAGTGTTCATTTAGAAACAAACCGAGTGGGCAACAGAA 240
Db 184 GGAAGGGGCTGGAGTGGGTCTCAGCTATTAG-----TGCTAGTGGTCATAGCATAT 237
QY 241 TAGCCGCGTCTGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAGCATCGCC 300
Db 238 TTGCGAGACTCCGTGAAGGCGCGGTTCACCATCTCCAGAGACAAATTCGAAGAACACGCTG 297
QY 301 TATCTCGAAATAGCAGCCTCGAAATCGAGGACACCGCCGCTTATTTACTGTACTACATCC 360
Db 298 TATCTCGAAATAGCAGCCTGAGAGCGAGGACACCGCCGCTATTTACTGTGCGA----- 352
QY 361 TACATTTTCATTTGTCGGGGTGTCTGCTATGAGGTTACTTCGAAATTCGGGGCCAG 420
Db 353 -AAGATCGAGAGGTTACTATGATAGTTGTACTTTAATGAGAGGCTTTGACTACTGGGCCAG 411
QY 421 GGCGCCCTGTGTACCCGTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCGCTGGCA 480
Db 412 GGAACCGGGTCAACCGTCTCTCCGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCA 471
QY 481 CCTCTCTCAAGAGCACCTCTGGGGCACAGCGGCCCTGGGCTGTGTCAGAGCACTAC 540
Db 472 CCTCTCTCAAGAGCACCTCTGGGGCACAGCGGCCCTGGGCTGTGTCAGAGCACTAC 531
QY 541 TTCCCGGAAACCGGTGAGCGTGTGTGAACTACAGGGCCCTGACAGGGCGGTGACACC 600
Db 532 TTCCCGGAAACCGGTGAGCGTGTGTGAACTACAGGGCCCTGACAGGGCGGTGACACC 591
QY 601 TTCCCGGCTGTCTCAGACTCTCAGACTCTACTCCCTCAGCAGCGTGTGACCGTGCC 660
Db 592 TTCCCGGCTGTCTCAGACTCTCAGACTCTACTCCCTCAGCAGCGTGTGACCGTGCC 651
QY 661 TCAGAGCTTGGGCAACCGACCTACATCTGCAACGTGAATCAAAAGCCAGCAACACC 720
Db 652 TCAGAGCTTGGGCAACCGACCTACATCTGCAACGTGAATCAAAAGCCAGCAACACC 711
QY 721 AAGGTGGACAAGAAAGCAGAGCCCAAACTCTGTGACAAATCTACATGCGCCACCGTGC 780
Db 712 AAGGTGGACAAGAGATGTTGAGCCCAAAATCTGTGACAAATCTACATGCGCCACCGTGC 771
QY 781 CCAGCACTGTAACTCTCTGGGGGACCGTCAGTCTTCTCTTCCCGCCAAAACCCAGGAC 840
Db 772 CCAGCACTGTAACTCTCTGGGGGACCGTCAGTCTTCTCTTCCCGCCAAAACCCAGGAC 831
QY 841 ACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCGTGAGCCAGAA 900
Db 832 ACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCGTGAGCCAGAA 891
QY 901 GACCCTGAGGTCAAGTTCACTGGTACGTGGAGCGGTGGAGGTGCAATAGCCAGACA 960
Db 892 GACCCTGAGGTCAAGTTCACTGGTACGTGGAGCGGTGGAGGTGCAATAGCCAGACA 951
QY 961 AAGCCGCGGAGGAGCAGTACAAAGCAGCTACCGTGTGGTCAGCGTCTCTCACCGTCTGT 1020
Db 952 AAGCCGCGGAGGAGCAGTACAAAGCAGCTACCGTGTGGTCAGCGTCTCTCACCGTCTGT 1011
QY 1021 CACCAAGGACTGCTCAATGGCAAGAGTACAAAGTCAAGGTCTCCAAAGCCCTCCCA 1080
Db 1012 CACCAAGGACTGCTCAATGGCAAGAGTACAAAGTCAAGGTCTCCAAAGCCCTCCCA 1071
QY 1081 GCCCGCCATCGAGAAACCATCTCCAAAGCCAAAGGGAGCCCGGAGACCAACAGGTGTAC 1140
Db 1072 GCCCGCCATCGAGAAACCATCTCCAAAGCCAAAGGGAGCCCGGAGACCAACAGGTGTAC 1131
QY 1141 ACCCTGCCCCATCCCGGATGAGTGAACCAAGAACCAAGGTGACCTGCTGCTGTC 1200
Db 1132 ACCCTGCCCCATCCCGGAGGAGATGACCAAGAACCAAGGTGACCTGCTGCTGTC 1191

QY 1201 AAAGCTTCTATCCAGGACATCCCGTGGAGTGGAGAGCAATGGCAGCCGAGAAC 1260
Db 1192 AAAGCTTCTATCCAGGACATCCCGTGGAGTGGAGAGCAATGGCAGCCGAGAAC 1251
QY 1261 AACTACAAGACCAAGCTCCCGTGTGAGTCCGACGGCTCTTCTTCTCTACAGCAAG 1320
Db 1252 AACTACAAGACCAAGCTCCCGTGTGAGTCCGACGGCTCTTCTTCTCTATAGCAAG 1311
QY 1321 CTACCGTGGACAAGAGCAGGTGGCAGCAGGGAAACGCTTCTCATGCTCCGATGATCAT 1380
Db 1312 CTACCGTGGACAAGAGCAGGTGGCAGCAGGGAAACGCTTCTCATGCTCCGATGATCAT 1371
QY 1381 GAGGCTCTGCACACCACTACACGACAGAGGCTCTCCCTGTCTCCGGTAAATGA 1437
Db 1372 GAGGCTCTGCACACCACTACACGACAGAGGCTCTCCCTGTCTCCCGGTAATGA 1428

RESULT 9
AAS22593
ID AAS22593 standard; cDNA; 1644 BP.
XX
AC AAS22593;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human cDNA encoding a novel human protein #159.
XX
KW Human; novel protein; ss; Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnary; nootropic;
KW anticonvulsant; antiarthritic; cerebrotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW thrombolytic; immunogen antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO200155437-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02623.
XX
PR 25-JAN-2000; 2000US-0491404.
XX
PA (HYSE-) HYSEQ INC.
XX
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-451939/48.
XX
PS P-PSDB; AAU14288.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage -
XX
PS Claim 1; Page 387-389; 894pp; English.
XX
CC The invention relates to polynucleotides encoding novel human
CC proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production.
CC The polypeptides are used to identify compounds which bind to the
CC polypeptides. Polynucleotides of the invention are used as probes and
CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to
CC target drugs to a tumour, in assays to determine biological activity, to
CC raise antibodies/elicit an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,


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Db 442 TAATCTGAATGAACAGCTGAGAGCTGAGGACACAGCGCTGTATTACTGTGGGARA--- 498
Qy 361 TACATTTACATTTGTGGGGTGTGTCTGTATATGAGGTTACTTCGAAATTTCTGGGCGCAG 420
Db 499 -GANGTTACTACTGTTTGGGAAAGCATCTACTACTACTTTTGAC-----TCTGGGGCCAG 550
Qy 421 GGGCCCTGTGTGCTCCTCCTCAGCTAGCACCAAGGGCCCATCGGTTCTTCCCTTGGCA 480
Db 551 GGAACMCTGGTCAACGCTCTCTCAGCTTCCACCAAGGGCCCATCGGTTCTTCCCTTGGCA 610
Qy 481 CCTCTCTCAAGAGACCTCTGGGGGACAGCGGCCCTGGGTCCTGTGTCAAGGACTAC 540
Db 611 CCTCTCTCAAGAGACCTCTGGGGGACAGCGGCCCTGGGTCCTGTGTCAAGGACTAC 670
Qy 541 TTCCCGAACCGGTGACGGTGTGTGTGAATCTCAGGCGCCCTGACCAAGCGCGGTGCACAC 600
Db 671 TTCCCGAACCGGTGACGGTGTGTGTGAATCTCAGGCGCCCTGACCAAGCGCGGTGCACAC 730
Qy 601 TTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCC 660
Db 731 TTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCC 790
Qy 661 TCCAGCAGCTTTGGGCAACCCAGACCTTACTATCTGCAACGTGAATCAAGGCCAGCAACAC 720
Db 791 TCCAGCAGCTTTGGGCAACCCAGACCTTACTATCTGCAACGTGAATCAAGGCCAGCAACAC 850
Qy 721 AAGTGTACAAGAAGACAGAGCCCAATCTTGTGACAAATCTACATGACATGCCACCGTGC 780
Db 851 AAGTGTACAAGAAGTGTGAGCCCAATCTTGTGACAAATCTACATGACATGCCACCGTGC 910
Qy 781 CCAGCACTGAATCTCTGGGGGACCGTCACTCTTCTTCCCTTCCCTTCCCTTCCCTTCCCT 840
Db 911 CCAGCACTGAATCTCTGGGGGACCGTCACTCTTCTTCCCTTCCCTTCCCTTCCCTTCCCT 970
Qy 841 ACCCTCATGATCTCCCGAACCCCTGAGGTCACTGCGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db 971 ACCCTCATGATCTCCCGAACCCCTGAGGTCACTGCGTGTGTGTGTGTGTGTGTGTGTGTGT 1030
Qy 901 GACCTGAGTCAAGTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
Db 1031 GACCTGAGTCAAGTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1090
Qy 961 AAGCGCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
Db 1091 AAGCGCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1150
Qy 1021 CACGAGGCTGGTGAATGGCAAGAGTACAAGTGAAGGTCTTCCAAAGCCCTTCCCA 1080
Db 1151 CACGAGGCTGGTGAATGGCAAGAGTACAAGTGAAGGTCTTCCAAAGCCCTTCCCA 1210
Qy 1081 GCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACCCACAGGTGTAC 1140
Db 1211 GCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACCCACAGGTGTAC 1270
Qy 1141 ACCCTGCCCCCATCCCGGATGAGCTGACCAAGAAACAGGTGAGCTGACCTGTGTGTGTGTGT 1200
Db 1271 ACCCTGCCCCCATCCCGGATGAGCTGACCAAGAAACAGGTGAGCTGACCTGTGTGTGTGTGT 1330
Qy 1201 AAAGGCTTCTATCCAGGCAATCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
Db 1331 AAAGGCTTCTATCCAGGCAATCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1390
Qy 1261 AACTACAGAACAGCCCTCCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
Db 1391 AACTACAGAACAGCCCTCCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1450
Qy 1321 CTCACCGTGGACAAGAGCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
Db 1451 CTCACCGTGGACAAGAGCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1510
Qy 1381 GAGGCTCTGCACAACTACACGAGAGAGCTTCCCTGTCTCCGGGTAAATGA 1437
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Db 1511 GAGGCTCTGCACAACTACACGAGAGAGCTTCCCTGTCTCCGGGTAAATGA 1567

RESULT 8
AAK98701
ID AAK98701 standard; cDNA; 1430 BP.
XX
AC AAK98701;
XX
DT 07-MAY-2002 (first entry)
XX
DE cDNA of the heavy chain of the monoclonal antibody from clone JA.
XX
KW HRIG; human rabies-immune globulin; monoclonal; virucide; heavy chain;
human monoclonal rabies virus neutralising antibody; immunoglobulin;
light chain; central nervous system; CNS; prophylactic therapy; clone JA;
ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
CDS 4..1428
FT /*tag= a
FT /product= "JA clone heavy chain protein"
XX
XX MO200188132-A2.
XX
XX 22-NOV-2001.
XX
XX 04-MAY-2001; 2001WO-US14468.
XX
XX 16-MAY-2000; 2000US-204518P.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Hooper DC, Dietzschold B;
XX
XX WPI; 2002-062381/08.
XX
XX P-PSDB; AAO14065.
XX
XX Novel isolated human monoclonal rabies virus neutralising antibody
XX useful for treating individual exposed to rabies virus and for
XX preventing spread of rabies virus to central nervous system -
XX
XX Claim 2; Page 22; 25pp; English.
XX
XX This polynucleotide sequence represents the cDNA of the heavy chain of
XX the monoclonal antibody from clone JA. The invention relates to an
XX isolated human monoclonal rabies virus neutralising antibody (virucide)
XX derived from cDNA clones encoding the antibody heavy and light chains
XX expressed in heterologous expression systems and purified away from
XX deleterious contaminants. The invention provides a fused gene encoding a
XX chimeric immunoglobulin light chain and a fused gene encoding a chimeric
XX immunoglobulin heavy chain. The antibody of the invention is useful for
XX treating an individual exposed to a rabies virus by administering to the
XX individual a therapeutically effective amount of the antibody, and
XX preventing a spread of the rabies virus to the central nervous system
XX (CNS). The antibody of the invention provides a safe and efficacious post
XX -exposure prophylactic therapy for individuals exposed to a rabies virus.
XX
XX Sequence 1430 BP; 326 A; 438 C; 396 G; 270 T; 0 other;

Query Match 82.5%; Score 1185; DB 24; Length 1430;
Best Local Similarity 90.1%; Pred. No. 2.4e-227;
Matches 1295; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

Qy 1 ATGGTTCGAGCCTCATCTGCTTCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 60
Db 4 ATGGAGTTTGGCTGAGCTGGCTTTTCTTGTGGCTATTTTAAAGGTGTCCAGTGTGAG 63
Qy 61 GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTTCAGCCTGGCGGGTCCCTGAGAGTCTCC 120
Db 64 GTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTGTACAGCCTGGGGGGTCCCTGAGAGTCTCC 123
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